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The role of Iron in Rheumatoid Arthritis

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A thesis submitted for the degree of Doctor of Philosophy
University of Bath
Department of Pharmacy and Pharmacology
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To my family ...

TABLE OF CONTENTS

Acknowledgements	V
Publications	VI
Abstract	VII
Abbreviations	VIII
<u>Chapter One – Introduction</u>	1
1.1 Inflammation	1
1.1.1 General Overview	1
1.1.2 Acute inflammation	2
1.1.3 Chronic inflammation	2
1.1.3.1 Rheumatoid arthritis	3
1.1.3.2 Osteoarthritis	4
1.2 Iron	6
1.2.1 General aspects	6
1.2.2 Iron Absorption	8
1.2.3 Iron homeostasis and metabolism	10
1.2.4 Iron and inflammation	13
1.2.5 Rheumatoid arthritis and Iron	15
1.3 Oxidative Stress	17
1.3.1 General overview	17
1.3.2 Free Radicals	17
1.3.3 Reactive oxygen species (ROS)	18
1.3.4 Reactive nitrogen species (RNS)	19
1.3.5 Oxidative stress in rheumatoid arthritis	19
1.3.6 Oxidative stress and the regulation of iron	20
1.4 Antioxidant defence system	22
1.4.1 Non-enzymatic antioxidants	22
1.4.1.1 Glutathione (GSH/GSSG)	22
1.4.1.2 Thioredoxin (TRx)	23
1.4.1.3 Ferritin (Ft)	24
1.4.1.4 Vitamins	27

1.4.2	Enzymatic antioxidants	27
1.4.2.1	Glutathione peroxidase (GPx) / Glutathione reductase (GR)	27
1.4.2.2	Superoxide dismutase (SOD)	28
1.4.2.3	Catalase	28
1.4.2.4	Haem Oxygenase (HO)	28
1.5	Lysosome	30
1.5.1	The role of lysosomal iron in oxidative stress	30
1.5.2	The role of lysosomal iron in rheumatoid arthritis	33
1.6	The NF-κB Transcription factor	34
1.6.1	The NF- κ B/Rel family	34
1.6.2	The I κ B family	35
1.6.2	The I κ B kinase (IKK) complex	35
1.6.3	NF- κ B activation pathways	35
1.6.3.1	The classical pathway	36
1.6.3.2	The alternative pathway	37
1.6.4	Redox regulation of NF- κ B	37
1.6.5	Oxidative stress and NF- κ B activation	38
1.6.6	NF- κ B and rheumatoid arthritis	39
1.6.7	The role of iron in NF- κ B activation	40
1.7	Aims and objectives of the project	41
	<u>Chapter two – Materials and Methods</u>	44
2.1	Chemicals and Reagents	44
2.2	Cell Culture	44
2.3	Treatments	45
2.4	MTT Assay	46
2.5	Flow Cytometric Analysis	47
2.6	Protein Measurements	47
2.7	Glutathione Measurements	48
2.8	Electrophoretic Mobility Shift Assay (EMSA)	48
2.9	Western blot analysis	50
2.10	Ferritin ELISA	51
2.11	Neutral red uptake assay	53
2.12	Lysosensor immunofluorescence	53

2.13 Immunocytochemistry	54
2.14 Preliminary clinical data	55
2.15 Labile iron pool (LIP) determination	57
2.16 Labile plasma iron (LPI) measurements	58
2.17 Statistical analysis of data	59
<u>Chapter three – Results</u>	60
Background	60
3.1 Determination of the sensitivity of J16 and HJ16 cell lines to H₂O₂	61
3.1.1 MTT assay	61
3.1.2 Flow cytometric analysis	63
3.2 The role of total intracellular glutathione (GSH/GSSG)	66
3.2.1 The effect of BSO treatment on J16 and HJ16 cell lines	66
3.2.2 The effect of BSO on the GSH/GSSG in J16 and HJ16 cell lines	68
3.2.3 Basal levels of the GSH/GSSG in J16 and HJ16 cell lines	68
3.2.4 The susceptibility of both cell lines to H ₂ O ₂ following GSH/GSSG depletion by BSO	72
3.2.5 Levels of total intracellular glutathione in J16 and HJ16 cell lines after the treatment of H ₂ O ₂	72
3.3 Characterisation of the response of NF-κB to H₂O₂	77
3.3.1 The induction of NF-κB complex in the J16 and HJ16 cell lines	77
3.3.2 Characterisation of the response of NF-κB and Oct-1 to H ₂ O ₂ treatment by immunocytochemistry	77
3.4 The role of labile iron	83
3.4.1 The role of LIP in differential sensitivity of the J16 and HJ16 cell lines to H ₂ O ₂ treatment	83
The source of iron in HJ16 cells following hemin treatment	92
3.4.2 The expression of HO-1 and HO-2 in Jurkat T cell lines	92
3.4.3 The levels of ferritin in Jurkat T cell lines	105
3.4.3.1 Basal levels of Ft in J16 and HJ16 cell line	107
3.4.3.2 Effect of H ₂ O ₂ on the Ft levels	107
3.4.3.3 Effect of DFO ± H ₂ O ₂ on the Ft level	109
3.4.3.4 Effect of hemin ± H ₂ O ₂ on the Ft levels	113
3.4.3.5 Effect of combined DFO/hemin ± H ₂ O ₂ on the Ft levels	116

3.4.3.6 Mitochondrial ferritin in the J16 and HJ16 cell lines	118
3.4.4 The role of iron-mediated lysosomal damage in J16 and HJ16 cell lines	118
3.4.4.1 Neutral red uptake assay	119
3.4.4.2 Lysosensor immunofluorescence	119
3.4.4.3 Cathepsin B immunocytochemistry	126
3.5 Preliminary clinical data	129
3.5.1 MTT assay	129
3.5.2 LIP measurements	129
3.5.3 LPI measurements	133
<u>Chapter four – Discussion</u>	136
Concluding Remarks and Limitations of this study	157
Further Directions	162
References	164

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PUBLICATIONS

1. Yiakouvaki A, Savovic J, **Al-Qenaei A**, Dowden J, Pourzand. Caged-iron chelators a novel approach towards protecting skin cells against UVA-induced necrotic cell death. *Journal of Investigative Dermatology*. 2006 Oct;126(10):2287-95.
2. Collins CA, Fry FH, Holme AL, Yiakouvaki A, **Al-Qenaei A**, Pourzand C, Jacob C. Towards multifunctional antioxidants: synthesis, electrochemistry, in vitro and cell culture evaluation of compounds with ligand/catalytic properties. *Organic & biomolecular chemistry*. 2005 Apr 21;3(8):1541-6.
3. **Al-Qenaei, A.**, Yiakouvaki, A., Hall, N. D., Pourzand, C. The role of lysosomal labile iron pool in differential sensitivity of Jurkat T cell lines to hydrogen peroxide *American Journal of Hematology*. 82 (6): 565-565 JUN 2007.

ABSTRACT

Iron plays a potential role in oxidative stress-mediated injuries and pathologies e.g. rheumatoid arthritis (RA). Four decades ago it was suggested that iron may have a crucial role in the progression of inflammation in RA. Indeed, free radicals generated by iron can cause damage to lipids, proteins, carbohydrates, and DNA. It is this destructive process that is believed to occur in rheumatoid joints. However, none had differentiated between the role of iron in both acute and chronic phases of the disease and the origin of this 'labile' iron. Since RA cells are chronically exposed to oxidative stress, we have therefore chosen Jurkat cells to be our cell model. We used the parental (J16) cell line was used to mimic the acute phase of oxidative stress and the H₂O₂-resistant (HJ16) cells to mimic the chronic phase. By using hydrogen peroxide (H₂O₂) as the oxidising agent, we aim to study the role of iron in acute and chronic phase of oxidative stress and to know its origin. In the present study, we found that both antioxidants and H₂O₂-induced labile iron are modulated when cells are chronically exposed to H₂O₂. HJ16 cells contain higher total intracellular glutathione levels and glutathione peroxidase activity than J16 cells while the superoxide dismutase and catalase activity are similar. Haem oxygenase-1 (HO-1) was not detectable nor was it induced in these cell lines; HO-2 on the other hand was expressed but not induced. Although they had the same 'basal' LIP and L-Ft levels, J16 cells contain more than 7-fold higher H-Ft levels than in HJ16 cells. It was also found that H₂O₂-induced labile iron is directly correlated with necrotic cell death. These results are consistent with the conclusion that both antioxidant defence mechanism and labile iron status are modulated in cells chronically exposed to H₂O₂. We have also shown that the 'basal' and 'H₂O₂-induced' NFκB activation was higher in the HJ16 cells. We have also provided a link between labile iron release, lysosomal membrane damage and the ensuing necrotic cell death following H₂O₂ treatment.

ABBREVIATIONS

AA	Adjuvant Arthritis
ADP	Adenosine 5'-diphosphate
AI	Anaemia of inflammation
ARD	Ankyrin repeat domain
ATP	Adenosine 5'-triphosphate
BSO	Buthionine-[S,R]sulfoximine
CA	Calcein
CA-AM	Calcein-acetoxymethyl ester
CIA	Collagen induced arthritis
CM	Condition media
CO	Carbon Monoxide
DFO	Desferrioxamine
DMEM	Dulbecco's Modified Eagle's Medium
DMSO	Dimethyl Sulphoxide
DMT1	Divalent metal transporter 1
DNA	Deoxyribonucleic acid
DTT	Dithiothreitol
EDTA	Ethylenediaminetetraacetic acid
EGTA	Ethylene glycol-bis[β -aminoethylether]-N,N,N',N'tetraacetic acid
EMEM	Earle's modified minimum essential medium
EMSA	Electrophoretic mobility shift assay
FAD	Flavin adenine dinucleotide
Fe²⁺	Ferrous iron
Fe³⁺	Ferric iron
Ft	Ferritin
GPx	Glutathione peroxidase
GR	Glutathione disulphide reductase
GSH	Glutathione (reduced)
GSSG	Glutathione disulphide (oxidised)

GSH/GSSG	Total intracellular glutathione
H	Hour / Hours
H-Ft	H-chain of Ferritin
H₂O₂	Hydrogen peroxide
HCP-1	Haem carrier protein-1
HEPES	N-[2-hydroxyethyl]piperazine-N'-[2-ethanesulfonic acid]
HO-1	Haem oxygenase 1
HO-2	Haem oxygenase 2
IL-1β	Interleukin-1 β
IRE	Iron-responsive element
IRP	Iron regulatory protein
RNS	Reactive nitrogen species
ROS	Reactive oxygen species
RT	Room temperature
L[•]	Fatty acid radical
LDL	Low density lipoprotein
L-Ft	L-chain of Ferritin
LIP	Labile iron pool
LI	Labile iron
LOO[•]	Fatty acid peroxy radical
LOOH	Lipid hydroperoxide
LPI	Labile plasma iron
MnSOD	Manganese superoxide dismutase
Mt-Ft	Mitochondrial ferritin
NADP	Nicotinamide adenine dinucleotide phosphate
NADPH	Nicotinamide adenine dinucleotide phosphate (reduced)
NBTI	Non-transferrin bound iron
NF-κB	Nuclear Factor kappa B
NLS	Nuclear localization sequence
NO	Nitric oxide
NO₂	Nitrogen dioxide
NP-40	Nonidet P-40
NR	Neutral red

OA	Osteoarthritis
O₂	Oxygen
¹O₂	Singlet oxygen
O₂⁻	Superoxide anion
OH[•]	Hydroxyl radical
PBS	Phosphate buffered saline
Pi	Inorganic Phosphate
PI	Propidium Iodide
PL	Picoliter
PMSF	Phenylmethanesulfonyl fluoride
PUFA	Polyunsaturated fatty acids
RA	Rheumatoid Arthritis
RHD	Rel-homology domain
ROS	Reactive oxygen species
RT	Room temperature
SDS	Sodium dodecyl sulphate
SF	Synovial fluid
SFM	Serum free media
SIH	Salicylaldehyde isonicotinoyl hydrazone
SOD	Superoxide dismutase
TCA	Trichloroacetic acid
Tf	Transferrin
TfR	Transferrin receptor
TNF	Tumor necrosis factor
TRx	Thioredoxin
UTR	Untranslated region
UV	Ultraviolet
V	Volts

CHAPTER ONE

INTRODUCTION

1.1 Inflammation

Inflammation has long been recognised both in clinical practice and in research laboratories (McCarty, 1989). The Roman physician Celsus (30 BC - 38 AD) described the classical signs of inflammation as 'redness' and 'swelling' with 'heat' and 'pain' (*rubor et tumor cum calore et dolore*). A century later, Galen (130-200 AD) added 'loss of function' (*function laesa*) to be the fifth sign of inflammation (Bonta *et al*, 1985 and Junqueira *et al*, 1986). Many of the classical features of inflammation were described as early as 1600 BC in Egyptian papyrus writings (Goldsby *et al*, 2003).

1.1.1 General overview

Inflammation is a term used to illustrate the body's complex physiological response, whether acute or chronic, to tissue injury (Underwood, 1996). It is a vascular and cellular defence reaction against foreign bodies; mainly pathogenic bacteria or chemical substances (Junqueira *et al*, 1986). This response is not a single event but rather a sequence of events to that particular injury (Bonta *et al*, 1985).

Injuries can be classified into three types: (i) physical injury, (ii) chemical injury, and (iii) pathogenic organisms. Physical injuries are those injuries that are related to trauma, radiation, heat, or cold. Chemical injuries are due to acid, alkalis, phenols etc, and pathogenic organisms such as bacteria, viruses or fungi can also cause injury to the exposed tissue (Mulvihill *et al*, 2001). In 1940, it was postulated that the endogenous release of substances was responsible for the characteristic changes seen in inflammation (Menken, 1940). Many years later, in a study performed by Spector and Willoughby (1957), it was shown that the first substance to be released was histamine in acute inflammation. After this discovery, other mediators have been postulated to be responsible for the initiation of inflammation, e.g. 5-hydroxytryptamine, bradykinin, and prostaglandins (Di rosa *et al*, 1971).

Depending on the duration of inflammation, it may be subdivided into acute and chronic inflammation. The transition from the acute to the chronic phase may be the result of three different factors (Bonta *et al*, 1985 and Goldsby *et al*, 2003) : (a) the persistence of the initiating inflammatory irritant (e.g. poorly degradable substance i.e. microorganisms possessing cell wall components that enable them to resist phagocytosis), (b) the presence of an endogenous antigen (e.g. modified protein is important in the development of adjuvant arthritis), or (c) various endogenous factors which alter the cell type and their function (e.g. mitogenic factors).

1.1.2 Acute inflammation

Acute inflammation is evident when the response of the microcirculation to tissue injury is a brief vasoconstriction of the arteriolar vessels which is then followed by vasodilatation (Bonta *et al*, 1985). Due to the release of histamine from mast cells, during acute inflammation, increased blood flow and capillary permeability occur along with the accumulation of fluid, leukocytes, and inflammatory mediators such as cytokines (Feghali and Wright, 1997). This produces oedema and in turn causes pressure on the nerves resulting in pain and loss of function. The role of this acute response is to clear dead cells from the site of the injury, to protect the site against any pathogens, and to permit the immune system to gain access to the site of inflammation (Junqueira *et al*, 1986).

Neutrophils predominate during this initial or acute phase, since they were principally present in acute inflammatory lesions (Stevens and Lowe, 1995). Acute inflammation usually begins within two hours of the injury and lasts for a couple of days. IL-1, IL-6, and TNF- α are cytokines which play a crucial role in the development of local and systemic features of the acute response (Goldsby *et al*, 2003).

Reactions to the skin from a burn or an insect bite, acute epiglottitis, acute meningitis, and acute hepatitis are various examples of acute inflammation.

1.1.3 Chronic inflammation

It is crucial that inflammatory reactions are self-limited upon e.g. elimination of the triggering factors, if not, they do perpetuate to chronic inflammation (Schett, 2008). The transition between the acute phase and the chronic phase is largely dependent on the persistence of the inflammatory cause. When the cause persists,

chronic inflammation follows, which may last for a prolonged duration of time - weeks, months, or even indefinitely, and subsequently the cell population changes (Feghali and Wright, 1997). Chronic inflammation can occur in three different scenarios: (1) when phagocytes are unable to degrade the microorganisms, (2) in an autoimmune disease in which self-antigens continually activate T cells, or (3) in cancer where the inflammation contributes to tissue damage (Goldsby *et al*, 2003).

Lymphocytes and macrophages are the predominant cells in chronic inflammation (Junqueira *et al*, 1986; Underwood, 1996; and Stevens and Lowe, 1999). In the inflamed area, these cells engulf the remains of cells and fibres and participate in the production of antibodies against invading microorganisms (Junqueira *et al*, 1986). Lymphocytes are the key components in the onset and exacerbation of autoimmune diseases and the cytokines produced by them have a great impact on disease progression (Horwood, 2008). Large numbers of activated macrophages release hydrolytic enzymes and reactive oxygen and nitrogen species which are responsible for the tissue damage observed in chronic inflammation (Goldsby *et al*, 2003). Cytokines released by activated macrophages are known to stimulate fibroblast proliferation and collagen production. IFN- γ and TNF- α , are the two central cytokines which play a central role in the initiation of this chronic response; IFN- γ is produced primarily by T cells whereas TNF- α is mainly produced by macrophages.

Examples of chronic inflammation would be: implanted foreign body in a wound, tuberculosis, inflammatory bowel disease (Crohn's disease and ulcerative colitis), and rheumatoid arthritis.

1.1.3.1 Rheumatoid arthritis

Rheumatoid arthritis (RA) is a chronic inflammatory and a systemic autoimmune disease of unknown aetiology, affecting 1-1.5 % of the world's population and involves all racial and ethnic groups (McCarty, 1989 and Khurana and Berney, 2005). It is an illness with significant mortality and morbidity rates due to organ damage and failure. The ratio of female to male patients is approximately 2-4:1, the basis of this difference is unknown (Khurana and Berney, 2005). Symmetric inflammation of synovial joints leading to progressive erosion of both articular cartilage and periarticular bone is its main characteristic (Doan and Massarotti, 2005 and Lipsky, 2007). Symptoms such as weight loss, fatigue, and malaise also occur in rheumatoid arthritic patients in addition to the articular manifestations (Khurana and

Berney, 2005). Rheumatoid arthritis is therefore a disease which combines chronic inflammation and bone loss; growing evidence shows that inflammation *per se* is a major precipitator for skeletal destruction (Schett, 2006).

Although the aetiology of RA is not known, it is believed to be related to a complex of genetic, endogenous (e.g. hormonal, endocrine, or metabolic factors), and exogenous factors (e.g. geographic, infectious agents, or occupational factors) (McCarty, 1989 and Doan and Massarotti, 2005). All have been shown to be implicated in the progress of RA but none is shown to be its primary cause.

Evidence coming from different experimental approaches (Panayi *et al*, 2001) strongly supports the hypothesis that RA is a disease initiated and driven by T cells irrespective of its cause. Macrophages, fibroblasts, and T lymphocytes are three cell populations which are found abundantly in the rheumatoid arthritic synovium (Tran *et al*, 2005); T-cells represent 40% of the synovial cellular infiltrate (Ling and Miossec, 2007). These cells are shown to play a substantial role in the development and the progression of RA (Cope, 2002). Stimulation of monocytes, macrophages, and synovial fibroblasts, by T-cells, leads to the secretion of a number of mediators including enzymes which are involved in the erosion and degradation of bone and cartilage. Along with this, these cells produce antibodies and proinflammatory cytokines (notably IL-1, IL-6 and TNF- α) that drive the chronic inflammation in RA (Doan and Massarotti, 2005 and Lipsky, 2007).

1.1.3.2 Osteoarthritis

Osteoarthritis (Weiland *et al*, 2005) is one of the most common musculoskeletal diseases and as in RA, the aetiology is largely unknown. It is characterised by the gradual development of pain, stiffness, and limitation of motion and these symptoms are localized in the joints (McCarty, 1989). It is therefore a painful and disabling disease that affects millions of patients around the globe i.e. every 1.5 minutes, a joint is replaced due to osteoarthritis (OA) in Europe. It mostly affects people above the age of 65, and inflammation can occur in OA but is more like a wear process, where the cartilage in the joint can't tolerate the load which has been placed on it. In RA by comparison, this process is a complication that only occurs later. Figure 1.1 shows an illustration of the cross section of a normal, RA, and OA knee joint.

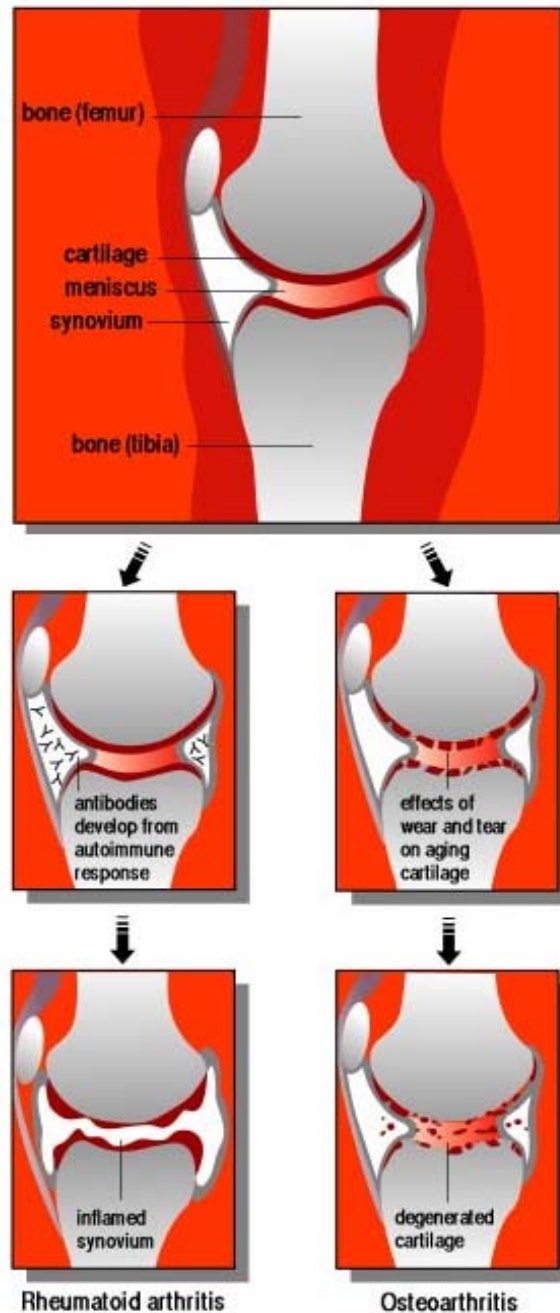


Figure 1.1 :

Cross section of a normal, RA, and OA knee joint.

The topmost illustration shows the cross section of a normal knee joint: a crescent-shaped disk held in place by ligaments (the meniscus) reduces friction during joint movement, while the membrane surrounding movable joints (the synovium) secretes a lubricating fluid.

Below that, the two illustrations on the left show the effect of rheumatoid arthritis, and the two illustrations on the right show the effects of osteoarthritis.

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1.2 Iron

The chemical symbol for iron, Fe, comes from the Latin word for iron – *ferrum*. Iron, with an atomic number of 26, is the second most abundant metal in the Earth's crust (aluminium is the most abundant metal).

1.2.1 General aspects

Iron is an essential element for nearly all living organisms by participating in a wide variety of important metabolic processes, such as oxygen transport (binding and release of haemoglobin), DNA synthesis, electron transport, lipid metabolism, photosynthesis and gene regulation (Lieu *et al*, 2001 and Cairo *et al*, 2006). Therefore, iron is indispensable for the living species. Under aerobic conditions, ferrous iron (Fe^{2+}) is readily oxidised in solution to give ferric iron (Fe^{3+}) which is insoluble at neutral physiological pH. As a result of this, iron has limited bioavailability (Papanikolaou and Pantopoulus, 2005) since environmental iron is in the ferric state (Syed *et al*, 2006).

Iron, in mammals, is a component of an iron storage protein (e.g. myoglobin and ferritin) and iron transport protein (e.g. haemoglobin and transferrin) (reviewed in Ganz and Nemeth, 2006) and the majority is present in the haemoglobin in erythrocytes (reviewed in Dunn *et al*, 2007). In humans, iron represents around 50 mg/kg in an adult man and because of increased blood loss during menstruation and child birth, around 40 mg/kg of total body weight in an adult woman (Worwood, 2005). Figure 1.2 shows a diagrammatic representation of iron distribution in the body (75kg man). Iron in circulating haemoglobin accounts for the largest component (nearly 80%). The remainder is mostly contained in ferritin and haemosiderin. Haemosiderin is the insoluble product of ferritin proteolysis in lysosomes (Halliwell and Gutteridge, 1999). Iron in myoglobin represents around 10%, with 1.3% in cytochromes and iron-sulphur proteins, and 0.1% in transferrin.

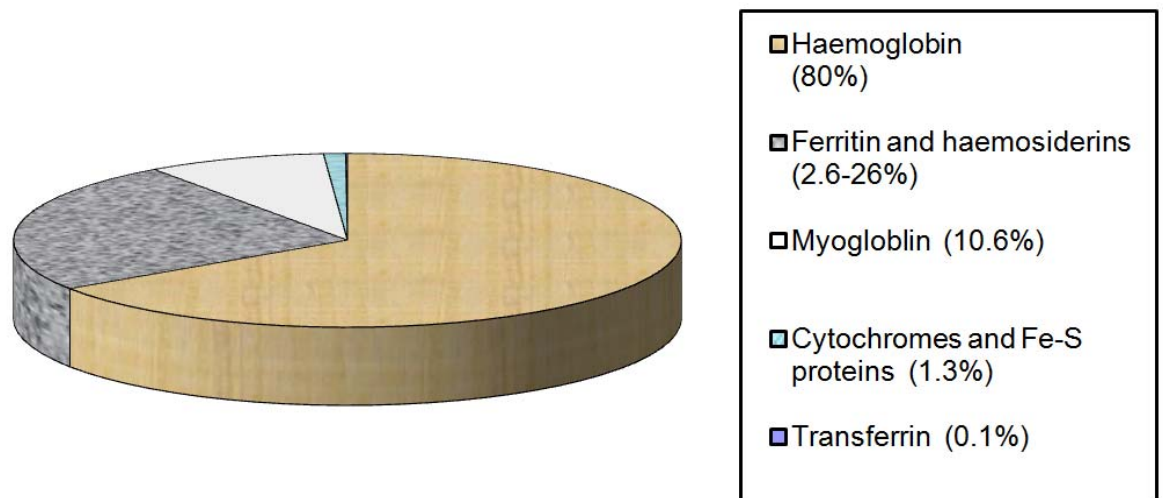


Figure 1.2:

Diagrammatic representation of iron distribution in the body

1.2.2 Iron Absorption

Due to epithelial shedding in the gastrointestinal tract and the skin and because of blood loss in women, around 1-2 mg of iron is lost on a daily basis. This loss is usually compensated by the absorption of iron through the diet which contains approximately 10-20 mg of iron of which 1-2 mg is absorbed under normal circumstances. This absorption is increased several fold when iron levels are low (e.g. in anaemia and hypoxia) and decreased when the iron stores are replete (e.g. in iron overload conditions and inflammation) (Andrews, 2005 and Ganz, 2007).

Dietary iron is absorbed in the duodenum by the duodenal enterocytes absorptive lining close to the gastro-duodenal junction (Andrews, 2000 and Miret *et al*, 2003). It consists of two components, haem and non-haem iron. Haem iron is exclusively present in animal tissues (e.g. in red meat), and is highly bioavailable and readily absorbed. Haem is a molecule that consists of protoporphyrin ring that binds ferrous iron. It results from the breakdown of haemoglobin and myoglobin found in meat products. Non-haem iron which is present in e.g. cereals and vegetables (and also in meat) is either in the reduced ferrous (Fe^{2+}) or mostly, in the oxidised ferric state (Fe^{3+}). Low pH in the gastric efflux facilitates iron absorption as it releases iron from ligands in food.

Haem enters the cell (see figure 1.3) via the haem carrier protein 1 (HCP-1) (Shayeghi *et al*, 2005) which is expressed in the apical membrane of duodenal epithelial cells, and inside the cell haem is degraded by haem oxygenase to yield ferrous iron (see section 1.4.2.4). The enterocytes of the luminal brush border contain an enzymatic ferric reductase activity, called Dcytb (the cytochrome *b*-like protein) (McKie *et al*, 2002), to ensure that non-haem iron is in the ferrous (Fe^{2+}) state since the bioavailability of iron is reduced when it is in the ferric state (Fe^{3+}). Along with the Dcytb, the presence of dietary reducing agents, such as ascorbate and small peptides containing cysteinyl and histidyl residues aid this reduction (Sharp, 2005). Divalent metal transporter 1 (DMT1, also known as Nramp2 and DCT1) is the apical major ferrous transporter, which is responsible for transporting iron into the cell. Other divalent metals such as Mn^{2+} , Cu^{2+} and Zn^{2+} are also transported by DMT1 (reviewed in Donovan and Andrews, 2004).

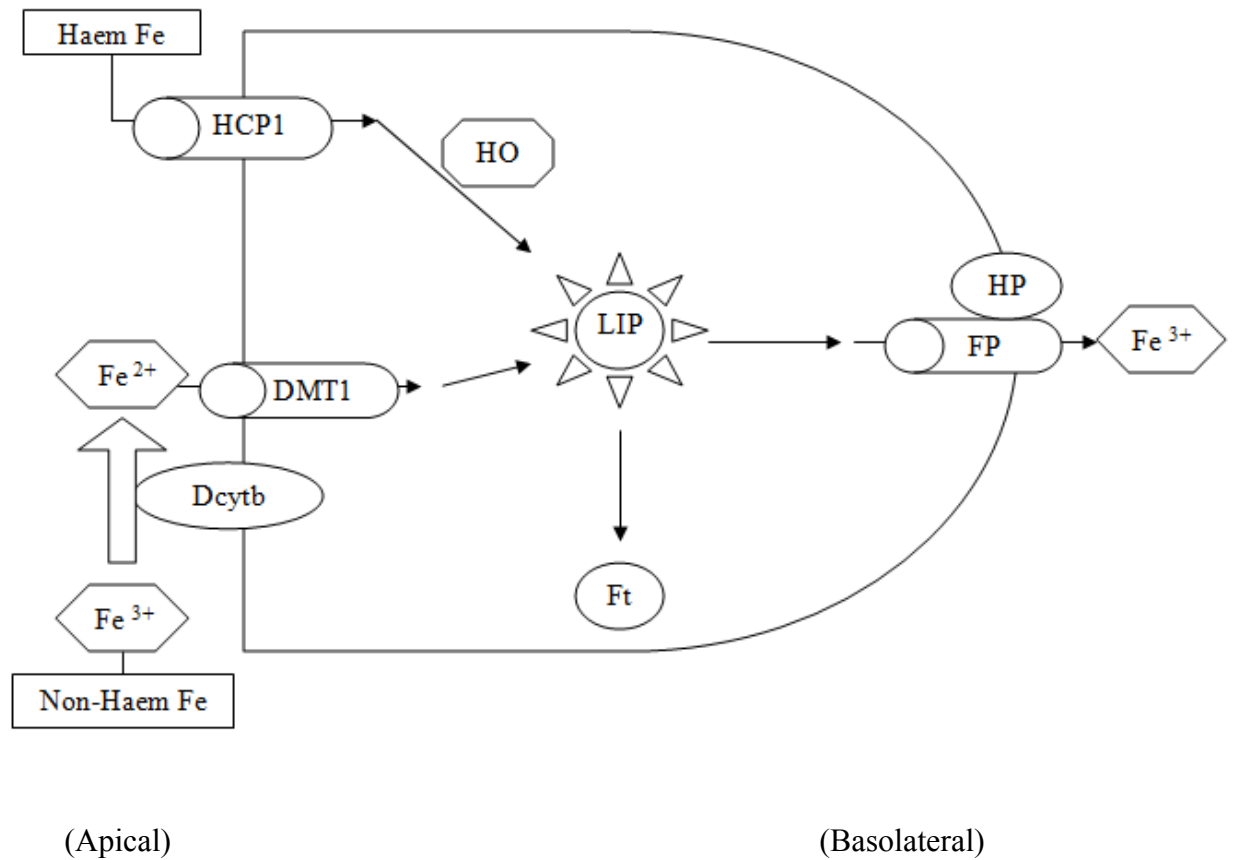


Figure 1.3:

The absorption of dietary iron by duodenal enterocytes.

Molecular pathways of haem and non haem iron absorption in the duodenum
(Modified from Sharp, 2005 and Syed *et al*, 2006)

Haem enters the cell via the HCP-1 which is expressed in the apical membrane of duodenal epithelial cells, and it is degraded by haem oxygenase to yield ferrous iron inside the cell. Iron enters the LIP where it may be then stored in Ft or transferred to the plasma and tissues by FP aided by HP, which exhibits a ferroxidase activity. The enterocytes of the luminal brush border contain an enzymatic ferric reductase activity, apparently the cytochrome *b*-like protein Dcytb, to ensure that non-haem iron is in the ferrous state since the bioavailability of iron is reduced when it's in the ferric state. DMT1 is the apical major ferrous transporter, which is responsible for transporting iron into the cell.

Abbreviation used: Dcytb, cytochrome *b*-like protein; DMT1, Divalent metal transporter 1; FP, ferroportin; Ft, ferritin; HCP1, haem carrier protein 1; HP, hephaestin; HO, Haem oxygenase; LIP; Labile iron pool.

Identified in 2000 by three groups (Abboud and Haile, 2000; Donovan *et al*, 2000; McKie *et al*, 2000), ferroportin (also known as IREG1 and MTP1) is a distinct transporter which is an excellent candidate for the basolateral transfer of iron to the plasma and tissues, although little is known how it transports iron (Ganz, 2007). Iron exports from intestinal cells appear to be aided by hephaestin, which exhibits a ferroxidase activity (i.e. converts Fe^{2+} to Fe^{3+}) required for such export (reviewed in Ganz and Nemeth, 2006) and ceruloplasmin is involved in iron export from non-intestinal cells. This notion is supported by the fact that hephaestin deficiency results in severe iron-deficiency anaemia (Anderson *et al*, 2002) and the deficiency of ceruloplasmin leads to iron accumulation in macrophages, hepatocytes, and cells of the central nervous system (Xu *et al*, 2004).

1.2.3 Iron homeostasis and metabolism

Although iron is indispensable for living organisms from bacteria to mammals (see 1.2.1), the tight control of this abundant transition metal metabolism is critical since disease is associated with both iron overload and deficiency (Andrews, 2000). Firm control of iron uptake, storage, and export is essential for cellular iron homeostasis (Hentze *et al*, 2004). It is normally controlled by the coordinate regulation of the expression of two proteins i.e. Ferritin (Ft) and transferrin receptor (TfR) (Harford and Klausner, 1990).

The presence of non-transferrin bound iron (NTBI) in the plasma of patients with iron overload disorders (e.g. thalassemia and haemochromatosis) and also in patients undergoing chemotherapy was first reported in 1975 (Hershko, 1975). However, still very little is known about its chemical nature. Following its receptor mediated uptake, NTBI causes organ dysfunction (Syed *et al*, 2006). Nevertheless, the majority of iron in the blood plasma of normal individuals and in the intestinal fluid is bound and transported by transferrin (Tf) (Klausner *et al*, 1993), that is an 80 kDa serum glycoprotein capable of binding a maximum of two atoms of ferric iron (Aisen and Listowsky, 1980). Plasma diferric Tf binds to the cell surface TfR, which is located on the surface of plasma membrane. The latter is a homodimer of 95 kDa that is capable of binding to two molecules of Tf. The Tf-TfR complex is then internalised by endocytosis. The endosome is then acidified and iron is exported to the cytosol via DMT1 (reviewed in Muckentahler *et al*, 2008), this results in the

release of ferric iron from the Tf and its subsequent reduction to ferrous iron. Iron is then utilised for the synthesis of iron-containing proteins and the excess is stored in the 440 kDa iron storage protein, ferritin. Cytosolic iron is stored in Ft in the ferric state but the mechanism of delivery is unknown. Recently, Shi *et al*, (2008) proposed that human poly (rC)-binding protein (PCBP1) can act as cytosolic iron chaperone in the delivery of iron to Ft. The remaining fraction of cytosolic iron usually stays in the cytosol weakly bound to low molecular weight ‘chelates’ such as citrate, ATP, pyrophosphates, and ascorbate. This fraction is accessible to iron chelators and therefore it is referred to as ‘chelatable iron’. The chelatable iron, which is in both ionic forms (Fe^{2+} and Fe^{3+}), is also known as the "labile iron pool" (LIP) (Jacobs, 1977 and Kakhlon and Cabantchik, 2002). The LIP, at normal levels, represents less than 5 % of the total cellular iron (Kakhlon and Cabantchik, 2002 and Andrews, 2004), but this portion changes with the iron status of the cell (reviewed in Arredondo and Nunez, 2005). The LIP reflects the iron status of the cell since it contains the cells' metabolically and catalytically reactive iron, therefore it is a marker of total iron content in the cells. The balanced movement of iron from extracellular and intracellular sources maintains the LIP. The Calcein (CA) assay is a simple and non-invasive fluorescent technique that is capable of measuring LIP in living cells (Epsztejn *et al*, 1997).

Transferrin has three major functions: (1) It allows ferric iron to remain soluble i.e. in aqueous and pH neutral plasma environment, (2) It allows iron to circulate in the safe form, and (3) It facilitates the cellular import of iron (Heeney and Andrews, 2004).

Ferritin (see section 1.4.1.3) is the principal site for iron storage and detoxification in microbial, plants, and animal species (Kuhn, 1994 and Aisen *et al*, 1999). In addition to its storage capacity, it serves as an iron source for haem synthesis and iron containing proteins, and it replenishes the LIP (Meyron-Holtz *et al*, 1999). The mammalian Ft is a heteropolymer of a combination of heavy (H) and light (L) chains of around 21 kDa and 19 kDa, respectively (Theil, 1987) which co-assemble to form a protein shell of 24 subunits. It can hold up to 4,500 iron atoms in its iron core that it surrounded by the shell, but usually has fewer. To store iron in Ft, several steps are required: (1) Fe^{2+} binding and migration to the ferroxidase site, (2) Fe^{2+} oxidation, (3) Fe^{3+} hydrolysis, and finally (4) nucleation and the core formation (reviewed in Harrison and Arosio, 1996 and Yang *et al*, 1998). The H-chain has a

ferroxidase capacity which is responsible for the rapid oxidation of ferrous iron to ferric iron and its incorporation. Therefore, the H-Ft has been proposed to be a regulator of the intracellular labile iron pool and a possible attenuator of oxidative stress in cells (Epsztejn *et al*, 1999). The L-chain contributes to the overall protein stability and is responsible for iron hydrolysis, nucleation, and the core formation (Lawson *et al*, 1989; Levi *et al*, 1992; Santambrogio *et al*, 1993; reviewed in Harrison and Arosio, 1996; Yang *et al*, 1998). Unlike H-Ft, L-Ft does not seem to have a major role in iron metabolism since subjects with genetic hyperferritinaemia-cataract syndrome have nearly 10-fold higher L-Ft than normal with no obvious abnormalities in iron metabolism (Beaumont *et al*, 1995 and Girelli *et al*, 1995).

Several studies have shown that the levels of iron co-ordinately control the levels of TfR and Ft. For example, during iron deficiency; the synthesis of Ft (L and H chain) will be brought to an end while the TfR expression is increased in mammalian cells therefore a higher number of TfRs will be present on their cell surface for internalisation. The opposite is true when iron is raised in culture medium; TfR is down regulated, whereas Ft synthesis is increased to remove excess iron (Kuhn, 1994 and reviewed in Cairo and Pietrangelo, 2000).

Levels of Ft and TfR are controlled by two mammalian iron regulatory proteins (IRP1 and IRP2), which are also the sensors of cytoplasmic labile iron (reviewed in Cairo and Pietrangelo, 2000). To ensure that the cells always contain sufficient iron for essential metabolic needs without exceeding the threshold of toxicity, intensive regulation of these proteins is essential (reviewed in Cairo *et al*, 2002). Adjustment of the intracellular iron concentration to normal and standard levels is mainly achieved by the use of these proteins at post-transcriptional levels, IRP-2 being the major sensor and modulator of iron metabolism (Recalcati *et al*, 2006). Iron-responsive elements (IRE) are stem loop structures with special base sequence in the mRNA of the Ft and TfR proteins (Theil 1990 and Eisenstein, 2000). In both H and L subunit of Ft, there is one IRE situated in the 5'- untranslated region (UTR), whereas TfR has five IRE motifs in its 3' UTR (Thomson *et al*, 1999). In iron-deficient cells, IRP-1 is activated by the removal of an attached iron-sulphur cluster and IRP-2's half life is prolonged which causes them to bind to the Ft's and TfR's IRE (Samaniego *et al*, 1994). The consequences of this binding complex are (1) inhibition of Ft mRNA translation and (2) the increase of the stability of TfR mRNA from nucleolytic degradation, therefore more protein is made. This will also increase the

translation of DMT1 and decrease ferroportin (reviewed in Muckentahler *et al*, 2008). Conversely, in iron replete cells, IRP-1 will be inactivated by its conversion to cytosolic aconitase (its physiological importance remains to be defined) and IRP-2 will be degraded subsequent to oxidation and ubiquitination (Iwai *et al*, 1998). This will cause (1) translation of mRNA encoding H and L Fts and (2) degradation of TfR mRNA. The lack of IRP binding activity will also decrease the translation of DMT1 and increase ferroportin (reviewed in Muckentahler *et al*, 2008). Thus, the IRP/IRE system (see figure 1.4) plays an important role for the regulation of Ft and TfR proteins (Eisenstein, 2000) and it has been suggested that this regulation is via the cytosolic LIP (Meyron-Holtz *et al*, 1999).

1.2.4 Iron and inflammation

During inflammation, T cells and macrophages produce a number of cytokines which influence the metabolism of iron; affecting its cellular uptake, transport, storage, as well as its absorption (Weiss, 2005). The induction of iron sequestration in macrophages and the decrease in iron absorption in the small intestine was shown in infections and inflammatory diseases. This results in the development of anaemia, termed ‘anaemia of inflammation’ (AI), formerly known as ‘anaemia of chronic disease’ (ACD).

The AI is a most common condition that is noticeable in patients suffering from inflammatory disorders (e.g. rheumatic diseases) (Konijn, 1994). It is characterised by low to normal serum iron levels (i.e. hypoferremia), low serum iron binding capacity, and normal to elevated ferritin concentrations. Several proinflammatory cytokines, such as IL-1 β and TNF- α , have been shown to contribute to the development of AI by the induction of hypoferremia. These cytokines cause a significant decrease in the low serum iron via the induction of Ft biosynthesis in macrophages (Alvarez-Hernandez *et al*, 1989 and Brock and Alvarez-Hernandez, 1989). They were also found to down-regulate TfR expression (Weiss, 2002) and to decrease Tf levels in patients with active RA and AI (Jongen-Lavernic *et al*, 1995). The up-regulation of DMT1 expression and the increase of iron influx into activated macrophages were shown by IFN- γ , LPS, and TNF- α . (Ludwiczek *et al*, 2003).

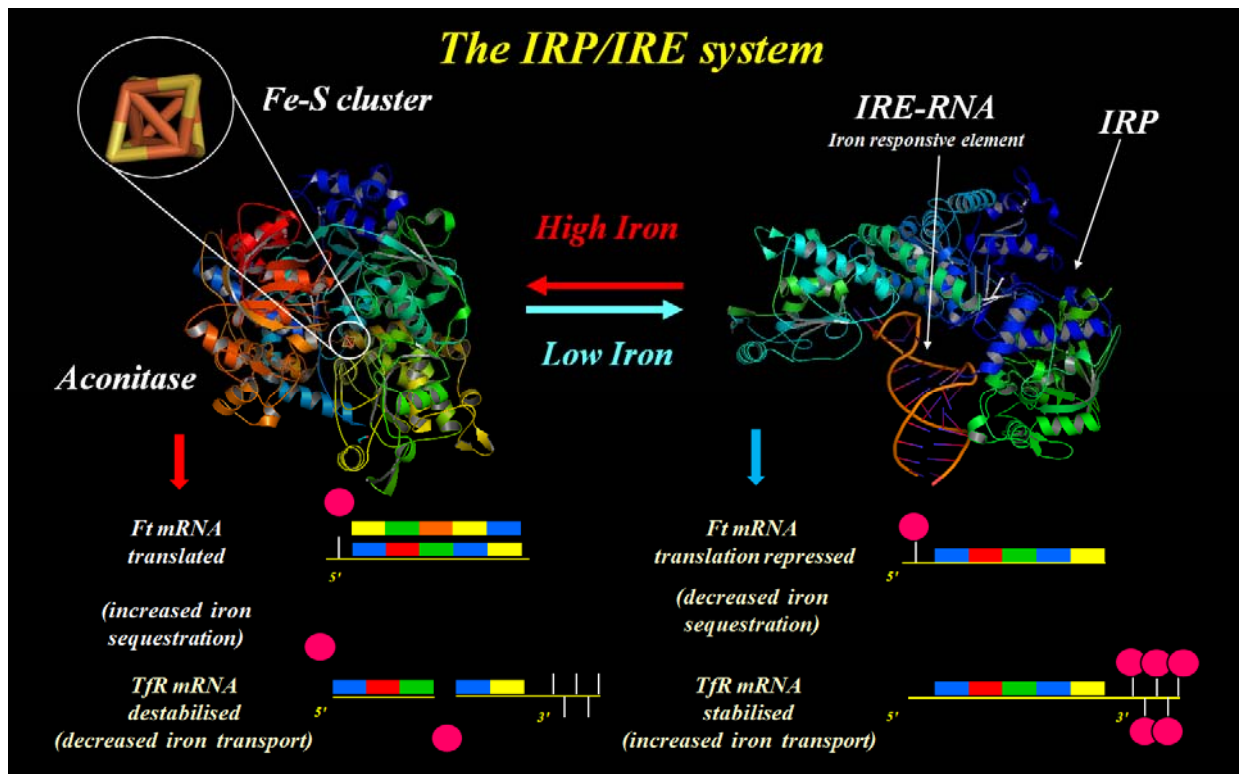


Figure 1.4 :

Illustration of the Iron regulatory proteins / Iron responsive elements system.

On the right, is a ribbon diagram of aconitase and on the left is a ribbon diagram of IRP bound to IRE. The pink circles on the right and the left represent the aconitase and IRP, respectively. The small white vertical lines on the 5' or the 3' region represent the IRE.

In iron deficiency, IRP binds to the IRE motifs of H- and L-Ft and TfR and therefore represses the translation of H- and L-Ft and stabilises TfR mRNA; leading to increased protein expression. Under iron excess conditions, IRP has low affinity for the IRE and instead has aconitase activity. This in turn leads to the translation of Ft and the destabilisation of TfR mRNA.

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Rheumatoid arthritic patients with anaemia had significantly higher serum levels of TNF- α , IL-1 and IL-6, when compared to non-anaemic RA patients (Voulgari *et al*, 1999). When macrophages were stimulated by IFN- γ and lipopolysaccharide (LPS), this induced nitric oxide (NO) synthesis and activated the IRP/IRE binding system (Weiss *et al*, 1993). Lipopolysaccharide, an endotoxin, is a component of the outer membrane of gram negative bacteria. Low intracellular iron is correlated with the production of NO which in turn decreases Ft synthesis and subsequently produces an increase in free iron (Weiss *et al*, 1994). It was recently demonstrated that T cells from RA patients produce > 2.5 times more NO than healthy donor T cells (Nagy *et al*, 2008). Since TNF- α increases NO production *in vitro* (e.g. in Jurkat cells), this indicates that the TNF- α induced NO production may contribute to RA disease progression.

Nemeth *et al*, (2004^a) showed that hypoferremia of inflammation is mediated by IL-6 inducing the synthesis of hepcidin, an iron-regulatory hormone. Hepcidin is a 25 amino acid polypeptide, with an antimicrobial action, produced mainly by hepatocytes, distributed in plasma and first isolated from the urine (reviewed in Ganz, 2003). During inflammation and infections, hepcidin is markedly induced causing the sequestration of iron in macrophages, hepatocytes and enterocytes (Ganz, 2005). It acts by inhibiting iron release from macrophages and from hepatic stores, and by inhibiting intestinal iron absorption. Hepcidin exerts its action by directly binding to ferroportin (FP) ; this binding causes the internalisation of FP and its degradation in the lysosomes (Nemeth *et al*, 2004^b). The loss of ferroportin from the cell membrane prevents cellular iron export. Acute and chronic inflammation and iron overload were shown to induce hepcidin synthesis, whereas anaemia and hypoxia suppress it (Pigeon *et al*, 2001 and Nicolas *et al*, 2002).

1.2.5 Rheumatoid arthritis and Iron

The potential role of iron in rheumatoid arthritis is well documented for the past four decades. *In vitro* studies revealed that ferrous ions in trace amounts were very active in the depolymerisation of purified hyaluronic acid and this is correlated with the low viscosity of synovial fluid (SF) of patients with RA. Spectrographic studies showed that SF from patients with RA contained elevated concentration of iron (Niedermeier *et al*, 1962). By emission spectrometric analysis, the mean concentration of iron was higher in the SF of RA patients than normal subjects

(Niedermeier and Griggs, 1971). Muirden and Senator (1968) were one of the first to suggest the critical role that iron could play in the pathogenesis of RA. In this study, their intention was to demonstrate the distribution of iron, using Prussian blue staining, in both normal and joint disease synovia. The staining occurred in all but one of the 23 rheumatoid arthritic synovia. On the other hand, all of the normal synovia showed a negative reaction with Prussian blue staining.

Proinflammatory cytokines such as TNF- α , IL-1, IL-6, and INF- γ , were shown to increase Tf and non-Tf bound iron uptake into human monocytes and increase Tf-bound iron uptake by synovial fibroblasts isolated from rheumatoid arthritic synovium (Telfer and Brock, 2004). This suggests that cytokines present in the rheumatoid arthritic synovium may lead to the accumulation of iron which contributes to the pathogenesis of the disease. Interestingly, TNF- α , IL-1, and IL-6 were also responsible for the induction of Ft synthesis in a hepatic cell line (reviewed in Torti and Torti, 2002).

Iron, mainly bound to Ft, is present in both the rheumatoid synovial membrane and fluid (Blake *et al*, 1981). In rheumatoid arthritic and osteoarthritic patients, iron concentration in the synovial tissue was significantly elevated (Ogilvie-Harris and Fornaiser, 1980). In RA, anaemia is the most frequent extra-articular manifestation of the disease. Its frequency in patients ranges from 15% to 80%, depending on the inflammatory condition. Nine of the eleven rheumatoid arthritic patients receiving iron dextran for the treatment of anaemia showed an exacerbation of synovitis (Blake *et al*, 1985). *In vitro*, iron dextran stimulates lipid peroxidation. As a result of this lipid peroxidation, it was suggested that iron dextran worsens synovial inflammation. Administration of desferrioxamine (DFO) to a chronic inflammatory animal model significantly decreased the chronic inflammatory phase (Blake *et al*, 1983). Desferrioxamine (DFO) is a chelating agent that has a high binding affinity for iron, it complexes one molecule of Fe³⁺ per molecule of DFO. Its advantage is in its capacity to chelate the 'free iron' inside the cell. It was therefore suggested that effective iron chelation and its removal may modify the inflammatory process in man. Desferrioxamine is also a weak scavenger of superoxide anion but a powerful one of hydroxyl radical and therefore it efficiently inhibits lipid peroxidation and protects cells against oxidative damage (Halliwell and Gutteridge, 1986). Also, when adjuvant arthritic rats were treated with DFO, the incidence and severity of joint inflammation was reduced (Andrews *et al*, 1987^a). It was also reported that mild iron deficiency

significantly reduces the severity of adjuvant induced joint chronic inflammation (Andrews *et al*, 1987^b). Taken together, these results suggest a potential role for iron in inflammatory joint disease notably rheumatoid arthritis.

1.3 Oxidative Stress

Oxygen is an element that exists in the atmosphere at the percentage of 21%, existing as a diatomic molecule, O₂, which is referred to as dioxygen. Oxygen has a pivotal role in all animals, plants, and bacteria, since it is essential for the production of energy by the use of the O₂ dependent electron transport. Experiments have shown that the O₂ will cause toxicity if given at a concentration higher than normal (Martinez-Cayueta, 1995).

1.3.1 General overview

“Oxidative stress” is a term introduced to illustrate the imbalance within the cells between the production of prooxidants and antioxidant defences in favour of the former. It occurs either from the increased production of reactive oxygen species (ROS) or reactive nitrogen species (RNS), or a deficiency in the antioxidant defence systems (Halliwell and Gutteridge, 1999 and Morel and Barouki, 1999).

1.3.2 Free Radicals

Any atom, molecule, or complex possessing an unpaired electron(s) and capable of independent existence is defined as a “free radical” (Cadogan, 1973). They can exist in either the gaseous or the liquid phase.

Free radicals can be formed by three independent methods:

- (a) Addition of a single electron: $A + e^{-} \longrightarrow A^{\bullet -}$
- (b) Loss of a single electron: $A \longrightarrow A^{\bullet +} + e^{-}$
- (c) Homolytic fission of a covalent bond where each pair possesses one of the unpaired electron: $A : B \longrightarrow A^{\bullet} + B^{\bullet}$

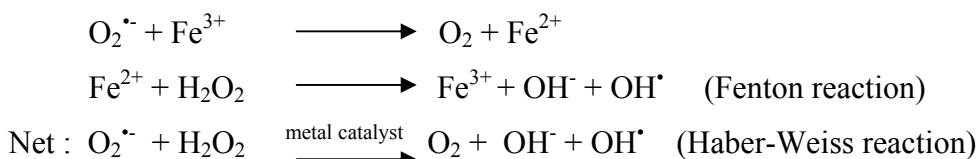
The primary source of the production of free radicals within the cells is the leakage of electrons, in the mitochondria and the endoplasmic reticulum, from the electron transport chain. Additionally free radicals are also produced by activated phagocytes (i.e. macrophages, monocytes, and lymphocytes) during inflammation (Cheeseman and Slater, 1993). In addition to these intracellular sources, there are

also exogenous sources such as ionizing radiation, tobacco smoking, and pollutants (Martinez-Cayueta, 1995).

1.3.3 Reactive oxygen species (ROS)

Reactive oxygen species (ROS) is a term used to include oxygen radicals and non-radical derivatives of oxygen. Superoxide anion radical ($O_2^{\bullet-}$) and hydroxyl radical (OH^{\bullet}) are examples of oxygen radicals, whereas hydrogen peroxide (H_2O_2) and singlet oxygen (1O_2) are examples of non-radicals.

Superoxide anion ($O_2^{\bullet-}$) is formed by the addition of a single electron to a dioxygen molecule, from about 1-3 % of the oxygen we breath in (Halliwell, 1994). The protonated form of the reduction of molecular dioxygen by two electrons is H_2O_2 . Both $O_2^{\bullet-}$ and H_2O_2 are produced by the NADPH oxidase which is located in the cell membrane. Singlet Oxygen (1O_2) is produced by a process which involves the input of energy to turn the two parallel spinning electrons into antiparallel spinning. The major source of the OH^{\bullet} is formed via the metal catalyzed Haber-Weiss or the Fenton reaction: Superoxide anion radical ($O_2^{\bullet-}$) converts ferric iron to ferrous ions and then ferrous ions react with H_2O_2 to produce OH^{\bullet} :



The most potent catalysts of OH^{\bullet} formation under normal physiological conditions are iron and copper ions (Halliwell and Gutteridge, 1999). The hydroxyl radical is more reactive than $O_2^{\bullet-}$ and H_2O_2 , possessing a short half life, while $O_2^{\bullet-}$ and H_2O_2 have longer half lives but are less reactive (Martinez-Cayueta, 1995).

All major cellular components may be injured by ROS. The cell membrane and the membrane of cell organelles (e.g. mitochondria, lysosomes, and peroxisomes) are rich in polyunsaturated fatty acids (PUFAs). Polyunsaturated fatty acids contain two or more carbon-carbon double bonds. The oxidative damage of PUFAs will result in lipid peroxidation; a free radical chain reaction that will generate fatty acid radical (L^{\bullet}) and consequently fatty acid peroxy radical (LOO^{\bullet}), and aldehydes (Cheeseman and Slater, 1993). In addition to rupturing the membrane and causing cell death, lipid peroxidation products can inhibit protein synthesis and block macrophage action (Winrow *et al*, 1993). Furthermore ROS can cause disturbances in proteins since they could react with amino acids such as histidine and cysteine.

Reactive oxygen species can also cause a cellular ion imbalance by attacking the proteins responsible for the maintenance of such balance (Halliwell and Gutteridge, 1999). In addition, DNA strand breakage has been demonstrated when cells were exposed to ROS, since OH^\bullet can damage sugars, purines, and pyrimidines. Carbohydrate damage has also been noticed in view of the fact that OH^\bullet in the presence of iron is responsible for the depolymerization of hyaluronic acid in vitro studies (Wong *et al*, 1981). The viscosity of synovial fluid within the joints is maintained by hyaluronic acid since it has lubricating properties.

1.3.4 Reactive nitrogen species (RNS)

Oxides of nitrogen such as nitric oxide (NO^\bullet) and nitrogen dioxide (NO_2^\bullet) are also free radicals which have the term 'reactive nitrogen species'. Nitric oxide (NO^\bullet) is formed *in vivo* from the amino acid L-arginine by three different NO-synthases (NOS) while NO_2^\bullet is made when NO^\bullet reacts with oxygen. They are both found in polluted air and smoke from the burning of organic material e.g. cigarette smoking. Peroxynitrite (ONOO^-) is often regarded as both a ROS and RNS, it is the reaction product of $\text{O}_2^{\bullet-}$ and NO^\bullet (Halliwell and Gutteridge, 1999) which are both produced from cells of the immune system during inflammation (Valko *et al*, 2007). Peroxynitrite (ONOO^-) is considered to be a potent oxidant and a major cytotoxic agent that can cause DNA fragmentation and lipid oxidation (Mladenka *et al*, 2006). In addition to ONOO^- , nitrous acid (HNO_2) and dinitrogen trioxide (N_2O_3) are examples of non-radical RNS.

1.3.5 Oxidative stress in Rheumatoid arthritis

Oxidative stress has been implicated in several physiological and pathological conditions (Vendemiale *et al*, 1999), such as atherosclerosis, diabetes, aging, rheumatoid arthritis, osteoarthritis, cancer, inflammatory bowel disease, and many more (Halliwell and Gutteridge, 1999 and Martinez-Cayueta, 1995). It is important to mention that the oxidative stress in many human diseases is a consequence and not a cause. In principle, disease-associated oxidative stress could result from either (or both): (1) decreased amount of enzymatic and non-enzymatic antioxidants (see section 1.4) and (2) increased production of ROS/RNS (see sections 1.3.3 and 1.3.4). For example during inflammatory processes, oxidative burst occurs (Halliwell *et al*, 1992) that is characterised by the massive production of ROS/RNS in that

environment which play a key role in defending cells against pathogens. The consequent increase in ROS/RNS leads to changes in signal transduction and gene expression; a common phenomenon seen in disease. Signal transduction (also called, cell signalling) is a process enabling information to be transmitted from outside the cell to various functional elements inside the cell and it is also the mechanism by which cells communicate with each other. Tissues often respond to mild oxidative stress by producing extra antioxidants, but severe oxidative stress can cause tissue injury and consequently cell death (Halliwell, 1994).

Several lines of evidence are in agreement with the concept that an 'oxidative stress' contributes to the pathogenesis of RA. Several studies have been suggesting that the rheumatoid synovium is relatively ischemic and that ischemia-reperfusion has been implicated to be major factor in the injury occurring in RA (Han *et al*, 2003). As ischemia-reperfusion occurs in the inflamed joint upon rest and movement, the authors suggest that it could be a potential target for the treatment of RA. During the isolation and stimulation of cells which are present in the inflamed joint (e.g. macrophages, neutrophils, and lymphocytes), the ability to produce ROS was noticed (Merry *et al*, 1989). T cell stimulation leads to the production of ROS and cytokines (reviewed in MacKenzie, 2006). Interestingly, also cytokines such as TNF- α and IL-1 lead to oxidant production (Finkel, 2003). In rheumatoid arthritic synovial lymphocytes, Remans *et al*, (2005) found intracellular ROS production. Hydrogen peroxide appears to be one of the ROS involved, since the addition of catalase (see 1.4.2.3) suppressed the intracellular ROS production. It was concluded that chronic oxidative stress observed in synovial T lymphocytes originates from intracellular ROS production. In other studies, Malondialdehyde (MDA) was measured as a marker of lipid peroxidation in rheumatoid arthritic patients and control subjects. The levels of plasma (Kamanli *et al*, 2004) and serum (Ozkan *et al*, 2007) MDA were significantly higher in patients with RA compared to the control. Recently Altindag *et al*, (2007) also demonstrated that DNA damage and total oxidative status was higher in patients with RA than in healthy controls and that total antioxidant status was lower in the same patients. It was therefore concluded in this study that the increase in lymphocyte DNA damage increase in patients with RA may be related to the increased oxidative stress and decreased antioxidant capacity.

1.3.6 Oxidative stress and the regulation of iron

Iron is an important element believed to generate oxidative stress i.e. an increase in the steady state concentration of prooxidants (e.g. by the formation of OH[•]) that damage membranes and DNA (Meneghini, 1997). The higher the LIP in the cells, the higher levels of ROS are noticed. Therefore, the LIP is not only a marker of the total Fe content in the cells but also determines the redox state of it.

Oxidative stress in the form of ultraviolet (UV) light has been shown to accumulate iron. Ultraviolet (UV) B radiation was shown to increase the skin level of non-haem iron (Bissett *et al*, 1991) and UVA radiation caused an immediate increase in 'free' iron in fibroblasts (Pourzand *et al*, 1999). When rat livers were exposed to oxidative stress in the form of phorone (a glutathione depleting drug), data suggests that there was an early increase in the levels of free iron pool (Cairo *et al*, 1995). Breuer *et al*, (1997) also showed that H₂O₂ induced a significant increase in LIP levels in cultured K562 cells. Iron deficiency is compensated by increased IRP activity which consequently results in the induction of TfR levels and reduced Ft synthesis, and therefore increases LIP levels (reviewed in Hentze and Kuhn, 1996). Stimulation of IRP activity by exposure of cells to H₂O₂ was shown in a number of studies (Pantopoulos and Hentze, 1995; Martins *et al*, 1995; Pantopoulos *et al*, 1996; Pantopoulos *et al*, 1997; Mueller *et al*, 2001). On the contrary, incubation of rat liver lysates with xanthine oxidase (which generates both superoxide anions and H₂O₂) revealed that a combined action of both H₂O₂ and O₂^{•-} were responsible to induce a reversible inactivation of IRP (Cairo *et al*, 1996 and Cairo *et al*, 1998). IRP inactivation by H₂O₂ and O₂^{•-} combination may serve as a protective mechanism against oxidative damage since it diminishes LIP before it converts H₂O₂ and O₂^{•-} into a potent oxidant. It has been demonstrated that H₂O₂ and O₂^{•-} can release iron from Ft (Rudeck *et al*, 2000 and Agrawal *et al*, 2001). Menadione-induced oxidative stress in B6 fibroblasts caused a post-translational inactivation of IRP (Gehring *et al*, 1999). IRP inactivity was also observed in rat subjected to ischemia-reperfusion, a process accompanied by a burst of ROS (Tacchini *et al*, 1997). There is therefore substantial evidence to conclude that the IRP proteins are targeted under conditions of oxidative stress in the cells (reviewed in Cairo *et al*, 2002). In a recent study, Andriopoulos *et al*, (2007) showed that sustained low levels of H₂O₂ up-regulated TfR1, leading to increased transferrin-mediated iron uptake and iron accumulation in the cells. Since IRP-1 was only partially and temporarily activated (likely because of H₂O₂ signalling)

the authors suggested that this effect is independent of IRP/IRE system. The lower biological reactivity of H_2O_2 (compared to many ROS) with its capacity to cross membranes makes H_2O_2 an ideal signaling molecule (Hampton and Orrenius, 1997). Indeed, it has been proposed that extracellular H_2O_2 seem to act through a membrane-transduced signaling process (reviewed in Cairo and Pietrangelo, 2000). Activation of IRP by H_2O_2 has been seen in intact cells but not in lysates (Mueller, 2005). Taken together, it seems that IRP responds in a different way to a variety of oxidative stress stimuli (Gehring *et al*, 1999).

1.4 Antioxidant defence systems

As previously mentioned, free radicals have been implicated in several physiological and pathological conditions. In addition they can cause protein oxidation, lipid peroxidation, carbohydrate damage, and DNA damage. Fortunately, our bodies acquire several defence mechanisms intended to prevent the damage or at least to minimize it.

Antioxidants are one of the major defence systems the body has acquired. An antioxidant is defined as “a substance that when present at low concentration compared to those of an oxidisable substrate significantly delays or prevents oxidation of that substrate” (Sies, 1997). There are considerable data to show their beneficial effects in animal models and clinical trials in the treatment of RA (Kunsch *et al*, 2005). Antioxidants can be divided into two categories; enzymatic and non-enzymatic antioxidants which can be found in both aqueous and membrane compartments within the cells.

1.4.1 Non-enzymatic antioxidants

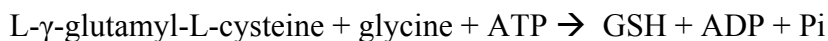
1.4.1.1 Glutathione

Glutathione (L- γ -glutamyl-L-cysteinyl-glycine) is a tripeptide molecule that is found in animals, plants, and many aerobic bacteria. In mammalian cells it is present in a millimolar range (Meister and Anderson, 1983) and it is the major cellular antioxidant. It is highly abundant in the cytosol (1-11 mM), nucleus (3-15 mM), and mitochondria (5-11 mM). It is synthesised by two steps (Halliwell and Gutteridge,

1999) as detailed below: First, the dipeptide formation is catalysed by γ -glutamylcysteine synthetase:



Then GSH is produced by glutathione synthetase:



Glutathione is present in two forms, the reduced form (GSH) and the oxidised form (GSSG) where it redox-cycles between them, but the vast majority (95-99%) is in the reduced form (Dethmers and Meister, 1981 and Meister and Anderson, 1983). In the cytosol and mitochondrial matrix, mammalian cells contain approximately 10 mM GSH and 0.5 mM GSSG (Droge *et al*, 1994). GSSG is synthesised by the addition of two GSH molecules with the oxidation of the –SH groups in cysteine to form a disulphide bridge (-S-S-) (Halliwell and Gutteridge, 1999).

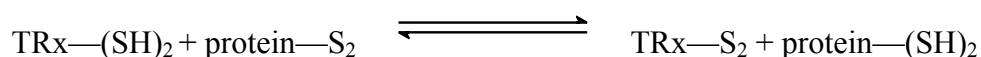
The glutathione system within the cells acts as a major homeostatic redox buffer and represents a primary antioxidant defence considering that it depends on the relative amounts of GSH/GSSG. Intracellular glutathione acts as an antioxidant in several ways. It can reduce peroxides to form H₂O (Martinez-Cayueta, 1995) or scavenge directly ROS (Cuzzocrea *et al*, 2004). It can also act as a chelator of Cu²⁺ and reduces its activity to generate ROS (Halliwell and Gutteridge, 1999). Glutathione, in yeasts, was found to play a major role in the maturation of cytosolic iron-sulphur proteins (Sipos *et al*, 2002).

Oxidative stress in the form of UVA radiation (oxidising component of sunlight, 320 - 380 nm) or H₂O₂ has been found to deplete intracellular glutathione (Lautier *et al*, 1992 ; Brunk *et al*, 1995^a ; Hempel *et al*, 1996). Treatments of Wistar rats with phorone, a glutathione depleting drug that amplifies the effects of ROS, induced Ft synthesis 6-fold in liver slices as a late response (Cairo *et al*, 1995). Recently, it was found that homocysteic acid, a glutathione depleting drug, increased the levels of H- and L-Ft mRNA (by nearly 2-fold) in HT22 murine hippocampal cells (Morozova *et al*, 2007). Exposure of mouse nerve cell line to glutamate blocks cysteine uptake and therefore depletes GSH, this leads to the accumulation of ROS and ultimately apoptotic cell death (Sagara *et al*, 1998). Several studies have shown that the depletion of intracellular glutathione sensitises cell populations to several circumstances such as aerobic ionising radiation, cytotoxic drugs, and H₂O₂. Indeed, glutathione depletion (by buthionine-[S,R]sulfoximine, BSO) sensitises cultured

human lymphoid cells against γ radiation (Dethmers and Meister, 1981), therefore it is regarded as a major protective agent.

1.4.1.2 Thioredoxin (TRx)

Thioredoxin is a thiol-polypeptide molecule that is present in mammalian cells. It is generally concentrated in the endoplasmic reticulum and also can be found on the cell surface. In addition to glutathione, TRx is also a major carrier of redox potential within cells (Kontou *et al*, 2004). They both maintain signalling components in a reduced state and are counterbalanced in signalling by oxidative stress, typically ROS (Jones *et al*, 2004). The term redox signalling is used to describe a regulatory process in which a signal is delivered through redox reactions (Valko *et al*, 2007). TRx has two –SH groups (reduced form) that is converted to an oxidised TRx with a disulphide (-S-S-). It undergoes redox reactions in the presence of proteins (Halliwell and Gutteridge, 1999).



Thioredoxin exerts its antioxidant activity by different pathways. It has been shown to possess a radical-scavenging activity (Schenk *et al*, 1994). It has been also involved in DNA repair, since it acts as a hydrogen donor for ribonucleotide reductase, which is an enzyme that is involved in the production of deoxyribonucleosides. It is also implicated in protein repair since it supplies methionine sulfoxide reductase with electrons. Methionine sulfoxide reductase repairs oxidative damage to methionine residues (Halliwell and Gutteridge, 1999). Thioredoxin levels in the synovial fluid and the synovial tissue of rheumatoid arthritic patients were elevated when compared with other joint diseases (Maurice *et al*, 1999). This observation suggests that synovial TRx may be a potential biomarker for RA (Kunsch *et al*, 2005).

1.4.1.3 Ferritin (Ft)

The ferritin molecule is a hollow protein shell (outside diameter around 13 nm, inside diameter around 8 nm), composed as mentioned in section 1.2.3, of heavy (H) and light (L) chains which co-assemble to form a protein shell of 24 subunits. Ratios of H-and L-Fts broadly differ from H^{24}L^0 to H^0L^{24} , these change in various diseases and under certain conditions (Halliwell and Gutteridge, 1999 and Theil,

2003). H-Ft is ubiquitous and contains a ferroxidase site, whereas L-Ft is catalytically inactive and unique to animals. Most intracellular iron is stored in Ft; it can store up to 4500 ion of iron (Halliwell and Gutteridge, 1999). In addition to iron, traces of other metals can be found in Ft including copper (Halliwell and Gutteridge, 1999).

Cairo *et al* (1995) have suggested that liver Ft can act as a pro- or an anti-oxidant in a time dependent manner. An early decrease in Ft has been shown after Wistar rats were treated with phorone, a glutathione depleting drug that amplifies the effects of ROS. Interestingly, 6-fold induction of Ft synthesis was shown as a late response. Treatment of skin fibroblasts with UVA lead to a total degradation of Ft (Pourzand *et al*, 1999). Six hours following UVA treatment, Ft levels returned to normal and increased up to 3-fold 24-48 hours following UVA treatment (Vile and Tyrrell, 1993). In endothelial cells, iron loading for 1 h significantly increased the cytotoxicity of H₂O₂ or oxidants from activated inflammatory cells (Balla *et al*, 1992 and Balla *et al*, 1993). Interestingly, at 16 h the cells became highly resistant to oxidative-mediated injury. This was correlated with 50-fold and 10-fold increase in haem oxygenase (HO) and Ft, respectively. The same phenomenon has also been seen in murine L1210 lymphocytic leukaemia cells using various types of oxidative insults (Lin and Girotti, 1997). Long exposure (i.e. 20-24 h) to hemin increased significantly the resistance of cells against H₂O₂- and ¹O₂-mediated toxicity. This resistance was correlated with 12- to 15-fold increase in H-Ft; L-Ft, on the other hand, was not modified. Iron loading of J774 macrophages increased the lysosomal iron content and their sensitivity to H₂O₂-induced (0.25 mM for 30 minutes) oxidative damage (Garner *et al*, 1998). However, after 24-72 hours, the cells were desensitised to the cytotoxic effects of H₂O₂. The resistance observed was linked to the lysosomal iron exocytosis and Ft synthesis. Therefore, it seems from the above studies that: in the early stages of oxidative challenge, Ft might act as a pro-oxidant molecule since its degradation could be a potential source of iron involved in the exacerbating the oxidative damage occurred in cells as a result of oxidative insult.

The evidence for Ft acting as an antioxidant molecule is also overwhelming (reviewed in Arosio and Levi, 2002). Various studies have reported that different forms of oxidative challenge have demonstrated an increase in Ft levels, conferring resistance to the subsequent insult. It was demonstrated that the ferroxidase sites in H-Ft significantly reduces the production of OH[•] from the Fenton reaction (Zhao *et al*, 2006). Induction of HO-1 by UVA radiation increases the Ft levels up to 3-fold 24-48

hours post-UVA radiation in human skin fibroblasts (Vile and Tyrrell 1993 and Vile *et al*, 1994). UV radiation has been shown to increase the Ft levels in both the epidermal and dermal tissue allowing increased protection against oxidative stress (Applegate *et al*, 1998). Hela cells, exposed to H₂O₂ treatment, increased the synthesis of H- and L-Ft and this overexpression in turn reduced the accumulation of ROS (Orino *et al*, 2001). It was suggested that Ft has an active role in regulating LIP levels and attenuating ROS generation in human erythroleukemia cells (Kakhlon *et al*, 2001). *In vivo* and *in vitro* studies, acute UVA exposure increased the expression Ft levels in basal epidermal cells (Siete *et al*, 2004). When human HL-60 leukaemia cells were pre-treated with hemin, they became more resistant to H₂O₂ and ¹O₂ toxicity (Lin and Girotti, 1998). This was correlated with 4 to 12-fold increase in Ft protein levels over a period of 24 hours. Bovine artery endothelial cells became sensitive to photodynamic therapy after 1 h treatment with hemin, but after 23 h they became more resistant (Lin *et al*, 1998). The hyperresistance to photodynamic therapy was correlated with the induction of H-Ft by hemin in these cells. The authors suggested that the enhanced oxidant resistance observed is due to the ability of Ft to rapidly sequester redox-active iron. Doxorubicin is an anticancer drug that generates ROS in H9c2 cardiomyocytes (embryonic rat heart-derived cell line) and promotes iron-catalysed oxidative damage (Corna *et al*, 2004). Through the action of ROS, it has also been shown that it increased H-Ft levels in these cells, and this has been correlated with the resistance to iron-mediated damage. Oxidised low density lipoprotein (LDL), an oxidant, dramatically stimulated L-Ft in the THP-1 macrophage line but failed to induce either H- or L-Ft in other studies (reviewed in Torti and Torti, 2002). L-Ft has been suggested to have an important role in the protection against oxidative damage due to the presence of antioxidant-responsive element (ARE) in the human L-Ft gene, which was positively regulated by hemin (Hintze and Theil, 2005). The ARE increases the expression of a diverse set of proteins involved in redox homeostasis such as TRx, HO and glutathione.

Levi *et al*, (2001) have described a gene that encodes a mitochondrial ferritin (MtF) located inside the matrix of the human mitochondria. Unlike other mammalian Fts, human MtF is a homodimer of 24 subunits that has a ferroxidase activity significantly lower than the H-chain cytosolic Ft (Bou-Abdallah *et al*, 2005). Iron is transported to the mitochondria for several metabolic processes, specifically haem and [Fe-S] cluster synthesis. Mitochondrial ferritin can efficiently store large

amounts of iron (1) to prevent its participation in Fenton reaction and (2) to protect the cell from iron being escaped during haem and [Fe-S] cluster synthesis. Since mitochondrial chelatable iron has been linked to several human diseases (e.g. Friedreich ataxia, Parkinson's and Alzheimer's disease), a new fluorescent indicator to determine this iron pool was synthesised (Petrat *et al*, 2002). During sideroblastic anaemia, large quantities of iron (due to the blockage of haem synthesis) and high levels of this new ferritin (MtF) appear to be present in the mitochondria. This suggests that MtF is responsible for the detoxification and the trafficking of iron in the mitochondria (reviewed in Arosio and Levi, 2002).

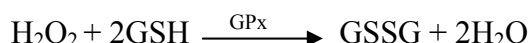
1.4.1.4 Vitamins

Antioxidant protection can also be achieved by vitamins that are available in our diet. Vitamin C (ascorbic acid) exerts its antioxidant levels by scavenging ROS i.e. $O_2^{\bullet-}$ and OH^{\bullet} . On the contrary, *in vitro* studies have shown that it has prooxidant properties as it acts as an iron reductant to produce OH^{\bullet} , but it has no major physiological relevance as any excess is simply excreted from the body (Halliwell and Gutteridge, 1999). The levels of vitamin C in human plasma were found to be around 10-100 μ M (Halliwell and Gutteridge, 1999). Good sources of vitamin C in our diet are vegetables and fresh fruits, especially tomatoes. It has very important roles in the body, in addition of functioning as an antioxidant, it regenerates vitamin E. In lipid peroxidation, vitamin E (a fat soluble vitamin) acts as an inhibitor of the free-radical reaction. Vitamin E has 8 members in its family, the best characterised is α -tocopherol. α -tocopherol, as well as inhibiting lipid peroxidation, it also acts as a scavenger of lipid peroxyl radicals (Cheeseman and Slater, 1993). Vitamin E may also act as a hydrogen donor to ROS, resulting in a less reactive species (Martinez-Cayueta, 1995). Green vegetables and cereal grains are excellent sources of vitamin E. α -tocopherol succinate pre-treatment protected cardiac myocytes against H_2O_2 - and $O_2^{\bullet-}$ -induced lysosomal damage (Roberg and Öllinger, 1998). α -tocopherol acetate was also involved in preventing UVA-mediated activation of NF- κ B that appeared to cause membrane damage to human skin fibroblasts (Vile *et al*, 1995 and Reelfs *et al*, 2004).

1.4.2 Enzymatic antioxidants

1.4.2.1 Glutathione peroxidase (GPx) / Glutathione reductase (GR)

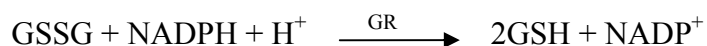
Glutathione peroxidase (GPx) and Glutathione reductase (GR) are present at high concentration in some parts of the human body i.e. liver, kidney, and whole blood. Glutathione peroxidase, first discovered in 1957, can be found in the cytoplasm and the mitochondria. It has four selenium atoms (Se), on its four protein subunits, which are responsible for its activity. Glutathione peroxidase catalyses the reduction of H_2O_2 yielding oxidised glutathione (GSSG):



It also catalyses the reduction of lipid hydroperoxides (Martinez-Cayueta, 1995):

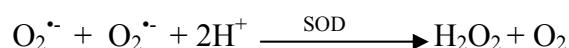


On the other hand GR contains flavin adenine dinucleotide (FAD), as its active site, on its two protein subunits. It is a cytosolic protein. Whilst the conversion of GSH to GSSG is high in normal cells (Halliwell and Gutteridge, 1999), GR acts by reducing oxidised glutathione to GSH.



1.4.2.2 Superoxide dismutase (SOD)

SOD exerts its activity to produce H_2O_2 and O_2 from the dismutation of $\text{O}_2^{\bullet-}$ (Martinez-Cayueta, 1995).

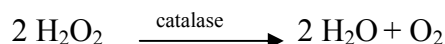


In mammalian cells three SODs are present: SOD1, SOD2 and SOD3 (Raha and Robinson, 2000). SOD1 is the cytosolic copper-zinc (CuZn) containing superoxide dismutase (or alternatively CuZnSOD), SOD2 is the intramitochondrial manganese (Mn) superoxide dismutase (or alternatively MnSOD), and SOD3 is the extracellular CuZn superoxide dismutase. Whereas SOD2 (MnSOD) is mostly present in the mitochondria, it is also present in the cytosol at a very low concentration (Halliwell and Gutteridge, 1999).

1.4.2.3 Catalase

Catalase is composed of four protein subunits, each of which have a ferric (Fe^{3+}) haem group bound to its active site (Halliwell and Gutteridge, 1999). It is present in all major body organs and at high concentrations in the liver. Catalase is

mainly located in the peroxisome, a cellular organelle found in the cytoplasm bound by a single membrane. As mentioned in the previous section, H_2O_2 is the product of the dismutation of $\text{O}_2^{\cdot-}$. Catalase removes the harmful effects of H_2O_2 (see section 1.3.3) by the following reaction (Martinez-Cayueta, 1995) :



1.4.2.4 Haem Oxygenase (HO)

Haem oxygenase (HO) is the rate limiting enzyme, found in the endoplasmic reticulum, that catalyses the degradation of haem (a pro-oxidant) and the formation of biliverdin and carbon monoxide (CO), and the release of ferrous iron ions (Halliwell and Gutteridge, 1999):



Biliverdin is then reduced, by biliverdin reductase, to produce bilirubin (an antioxidant). With a decrease in the pH, the potency of bilirubin as a free radical scavenger is increased (Winrow *et al*, 1993). All three discrete products (i.e. Fe^{2+} , CO, and biliverdin-bilirubin) have vital physiological roles which may be complementary (Snyder and Baranano, 2001). Depending on the cellular redox potential and the metabolic fate of haem iron, HO may have both pro- and antioxidant properties (Ryter and Tyrrell, 2000).

To date, three haem oxygenase isozymes have been identified: HO-1, HO-2 and finally HO-3. HO-1 (the inducible form) and HO-2 (in general; the constitutive form) isozymes are both known to be haem catalyst (Maines *et al*, 1986), HO-3 has a poor haem catalyst activity (Wunder and Potter, 2003). Out of the three, HO-3 is less understood; it is thought to serve primarily as a haem-binding protein (McCoubrey *et al*, 1997 and Weng *et al*, 2003).

While HO-2 is believed to be the constitutive form of HO, HO-1 is a stress-induced enzyme (Keyse and Tyrrell, 1989) which is activated by a number of stimuli such as UV radiation and H_2O_2 in human skin fibroblasts. Since HO-1 mRNA is strongly induced by ROS, this makes it a potential marker for cellular oxidative stress at the mRNA level. It has been proposed that H_2O_2 formation during mitochondrial respiratory chain deficiency (a pro-oxidant state) leads to the overexpression of antioxidant enzymes; GPx activity, GPx and HO-1 mRNAs (Brambilla *et al*, 1997). Glutathione depletion by BSO treatment of human skin fibroblasts lead to a

significant increase in the level of HO mRNA (Lautier *et al*, 1992). It was also 10-fold higher 24 h after either UVA or H₂O₂ treatment. Synthesis of HO-1 but not HO-2 was shown to be induced by glutathione depletion in Chinese hamster ovary cells (Saunders *et al*, 1991). Glutathione depletion also induced HO-1 protein and mRNA in rat brain (Ewing and Maines, 1993). Interestingly, HO-1 was most expressed in the lesions of synovial tissue of patients with RA than in those from the other patient groups (osteoarthritis, and patients with noninflammatory joint disease). Both hemin and auranofin (a disease-modifying antirheumatic drug) induced HO-1 and reduced expression of TNF- α mRNA, LPS-induced secretion of IL-6 and IL-8, and expression of cyclooxygenase 2 in the synovial cell lines (Kobayashi *et al*, 2006).

As mentioned earlier (see section 1.4.1.3), induction of HO-1 by UVA radiation increases the Ft levels up to 3-fold 24-48 hours post-UVA treatment in human skin fibroblasts (Vile and Tyrrell 1993 and Vile *et al*, 1994). The photoimmunoprotective activity of UVA radiation seen in mice has been attributed to the HO induction (Reeve and Tyrrell, 1999). A strong relationship between HO induction and photoimmunoprotection by UVA has been established (Reeve and Domanski, 2002). Cells overexpressing HO have shown hypersensitivity to UVA shortly after hemin treatment (Kvam *et al*, 2000). These cells were no longer hypersensitive to UVA, 24 hours post-hemin treatment. It has also been found that HO-1 is linked to the efflux of iron from the cells, therefore it was suggested that its induction prevents cell damage and death by regulating cellular iron (Ferris *et al*, 1999). Therefore, the HO system has been implicated in antioxidant, anti-inflammatory, and cytoprotective events (Taramelli *et al*, 2000; Ryter and Tyrrell, 2000; Tranter and Jones, 2008).

1.5 Lysosome

Lysosomes were first isolated by Christian de Duve and colleagues in rat liver, later they were found to exist in a variety of cells and tissue (De Duve and Wattiaux, 1966) including animal and plant cells. They are membrane bound organelles filled with around 40 types of hydrolytic enzymes, including cathepsins, proteases, nucleases, lipases, and phospholipases. These enzymes are active under acidic condition (pH around 5.0) and this is maintained by an ATP driven H⁺ pump located in the lysosomal membrane (Alberts *et al*, 2002). Lysosomes mainly serve as sites for

degradation in the cell and a centre for normal turnover of organelles; it is also the major site of intracellular catabolic processes (Sriram *et al*, 2006).

1.5.1 The role of lysosomal iron in oxidative stress

In animal cells, Ft is consistently found in the cytosol and lysosomes (reviewed in Harrison and Arosio, 1996). The lysosomal degradation of metalloproteins (e.g. cytochromes) and ferruginous material (e.g. Ft) ensures the intralysosomal availability of redox-active low-molecular-weight chelatable iron i.e. LIP (Ciechanover, 2005). By laser scanning microscopic study, chelatable iron was found to be 2-3 fold higher in the endosomal/lysosomal apparatus than in the cytosol of isolated rat hepatocytes and rat liver endothelial cells (Petrat *et al*, 2001). Therefore a major part of the LIP might be present in the lysosomes (Kakhlon and Cabantchik, 2002). This, along with the OH[•] produced by Fenton reaction, accounts for the sensitivity of lysosomes to oxidative stress. Also, since the lysosomal environment is acidic it facilitates the release of iron from proteins and it enhances its reduction to ferrous iron, therefore the oxidative damage is enhanced.

Treatment of macrophage-like J-774 cells with a bolus dose of 0.5 mM H₂O₂ caused lysosomal damage and plasma membrane blebbing as an early sign of damage (Brunk *et al*, 1995^b). These effects were prevented by pre-treatment with DFO, which is taken up by endocytosis and stored intralysosomally. DFO, being a hydrophilic compound, has limited cellular penetration (Rice-Evans *et al*, 1989 and Link *et al*, 2003) therefore it enters the cells by endocytosis and finally accumulates in the lysosomes (Lloyd *et al*, 1991 and Cable and Lloyd, 1999). When the cells are not exposed to the drug anymore, DFO can then slowly leave the lysosomal compartment, reaching the cytosol and subsequently the extracellular fluid. The protective effects of DFO were prevented by the inhibition of its endocytosis. Lipid peroxidation, destabilisation of lysosomes, and eventually cell death were seen when rat hepatocytes were treated with naphthazarin, a redox-cycling drug which mainly exerts its toxicity through oxidative stress (Öllinger and Brunk, 1995). Pre-treatment with DFO protected the cells from lysosomal destabilisation and cell death. Exposure to a low steady state of H₂O₂ (25 µM) in Jurkat T cells induces apoptosis, which is consequence of lysosomal rupture (Antunes *et al*, 2001). Pre-exposure to DFO preserved lysosomal stability and consequently protected the cells from apoptosis. Ogawa *et al*, (2004) have shown that ROS formation was augmented in the

mitochondria and the lysosomes of irradiated T cells in the presence of a low concentration of H_2O_2 (0.1 mM) when compared with those treated only with irradiation. Both lysosomal and cellular damage were prevented when cells were pre-treated with the lipophilic chelator salicylaldehyde isonicotinoyl hydrazone (SIH) and/or DFO prior to their exposure to H_2O_2 , since LIP was efficiently decreased (Kurz *et al*, 2006).

When human fibroblasts were irradiated with a moderate dose of blue light, this (moderate) stress of photo-oxidation resulted in apoptosis (Brunk *et al*, 1997). The blue light-mediated damage appears to be accompanied by leakage of lysosomal contents including hydrolytic enzymes, such as cathepsin D (CATH D) (Roberg and Öllinger, 1998). Severe photo-oxidation, on the other hand, results in severe lysosomal damage and consequently cellular necrosis, therefore the cascade of events is dependent on the magnitude of the insult. Treatment of macrophages with oxidised LDL induced lysosomal destabilisation, relocation of CATH D to the cytosol, and increased cathepsin L (CATH L) cytosolic activity (Li *et al*, 1998). During lysosomal membrane permeabilisation, cathepsin B (CATH B) and CATH D have been documented to be released from the lysosomes (Erdal *et al*, 2005). Treatment of human skin fibroblasts with UVA radiation (320 – 380 nm) lead to an immediate release of iron via the proteolysis of Ft (Pourzand *et al*, 1999). This study provided the first evidence that UVA-mediated Ft degradation originates from the destabilization of lysosomal membranes and the subsequent leakage of proteolytic enzymes. Chymotrypsin, a lysosomal protease that is responsible for the degradation of Ft molecules in lysosomes, was around 3-fold higher in the cytosolic fraction of UVA-treated cells when compared with unirradiated controls. The degradation of Ft was prevented when cells were pretreated with Chymotrypsin-specific lysosomal protease inhibitors (i.e. Chymostatin and Leupeptin). Delocalisation of CATH B from the lysosomal compartment to the cytosol was observed after UVA radiation in human skin fibroblasts (Basu-Modak *et al*, 2006). When human skin fibroblasts were pre-treated with catechins (flavonoid constituents with protective properties predominantly against oxidative stress) prior to UVA-radiation; iron release was prevented (Basu-Modak *et al*, 2006). Based on measurements of lysosomal integrity (Lysosensor assay and CATH B immunocytochemistry), the data strongly indicate that catechins protect against lysosomal damage induced by UVA. 40 Gy radiation of radio-resistant lymphoma (J774) cells increased the ‘loose’ iron by nearly 5-fold

(Persson *et al*, 2005). This increase was correlated with lysosomal rupture and consequent cell death following a second dose of 20 Gy. Addition of DFO before the first or second radiation stabilised the lysosomal membrane and largely prevented cell death. Cytochemical analysis from this study revealed that the most redox-active iron lies within the lysosomes. Unless catalytically active iron is present, neither superoxide radicals nor H_2O_2 induced any lysosomal damage by themselves in lysosome-enriched mitochondrial fraction of a rat liver homogenate (Zdolsek and Svensson, 1993). Overall, these results support the idea that oxidative stress *per se* is not injurious but it requires the presence of intralysosomal redox active iron (reviewed in Terman *et al*, 2006).

1.5.2 The role of lysosomal iron in rheumatoid arthritis

Lysosomes are abundant in the lining cells of the synovial membrane. There is a considerable amount of evidence to support that lysosomal membrane damage is linked to acute and chronic inflammation in joints. The lysosomal membrane contains large amount of PUFAs (see section 1.3.3) that are susceptible to lipid peroxidation. When lipid peroxidation occurs the membrane is disrupted and this releases hydrolytic enzymes which will potentiate inflammation (Blake *et al*, 1981). Increased lysosomal enzyme activity has been found in the synovial fluid and membrane in RA. It is evident that materials in lysosomes can provoke inflammation, tissue injury and breakdown of connective tissue (Weissmann, 1972).

It was concluded that the extensive tissue breakdown in adjuvant arthritis is due to the release and degradative action of lysosomal enzymes on connective tissue components (Anderson, 1970). Administration of two non-steroidal anti-inflammatory was found to increase the lysosomal stability in adjuvant arthritic rats (Reddy and Dhar, 1987). Oral administration of several anti-inflammatory drugs such as phenylbutazone and hydrocortisone decreased both the enzymatic activity and oedema. The study concluded that these drugs may act by inhibiting lysosomal enzyme, stabilising cell or lysosomal membrane, or decreasing influx of leucocytes. In patients with RA, high enzyme levels were found and this was correlated with damage to the joints (Muirden, 1972). In all patients with RA, elevated cysteine protease CATH B, dipeptidyl peptidases I, aspartate protease CATH D and two glycosidases were found (Sohar *et al*, 2002). The magnitude of the increased activity was correlated with duration of the disease.

Recently, *Cleome gynandra* was found to markedly decrease lysosomal enzymes in both the plasma and the liver of adjuvant-induced arthritic rats (Narendhirakannan *et al*, 2007). *Cleome gynandra*, a common weed which grows in tropical countries, is commonly used to treat rheumatism. It was proposed that *Cleome gynandra* might exert its anti-inflammatory actions by stabilizing the lysosomal membrane and thereby preventing the release of lysosomal enzymes. The above findings support the concept that lysosomal enzymes are involved in connective tissue damage and that lysosomes play a crucial role in the pathogenesis of RA.

1.6 The NF- κ B transcription factor

Nuclear Factor κ B (NF- κ B) is a transcription factor that was first discovered in 1986, as a nuclear factor that binds to a site in the immunoglobulin κ light chain enhancer in B cells only, hence its name (Sen and Baltimore, 1986). Within a few years, it was found that NF- κ B is present virtually in all cell types. The NF- κ B regulates the transcription of many genes involved in immune and inflammatory responses, and apoptosis (Ghosh and Karin, 2002). The activation of NF- κ B has been implicated in various diseases (Baldwin, 2001) e.g. rheumatoid arthritis, cancer, AIDS, inflammatory bowel disease etc. The NF- κ B is a dimer of proteins that belongs to the NF- κ B/Rel family.

1.6.1 The NF- κ B/Rel family

In mammalian cells the NF- κ B/Rel family consists of 5 members; RelA (p65), RelB, c-Rel, p50 (NF- κ B 1), and p52 (NF- κ B 2). The first three are produced within the cells as transcriptionally active proteins, whereas p50 and p52 are generated from p105 and p100, respectively, by proteolytical degradation (Mercurio and Manning, 1999). They can form homo- and hetero-dimers with each other but certain dimers do not exist i.e. RelB can only hetero-dimerise with p50 or p52 (Ryseck *et al*, 1995). The “classical” NF- κ B dimer is RelA/p50 given that it is the most abundant and biologically active within the cells, and it was also the first form to be identified (Huxford *et al*, 1998 and Karin and Ben-Neriah, 2000).

This family possesses an N terminal region of around 300 amino acids called the Rel-homology domain (RHD), hence the family’s name. The RHD is responsible

for dimerisation with other member of the same family, nuclear translocation since it has a nuclear localization sequence (NLS), DNA binding, and the interactive domains of the inhibitory I κ B proteins (Siebenlist *et al*, 1994).

1.6.2 The I κ B family

Members of this family include I κ B α , I κ B β , I κ B γ , I κ B ϵ , p100, p105, and Bcl-3. They contain six to eight ankyrin repeat domains (ARD) which are 33 amino acids in length (Siebenlist *et al*, 1994). These ARDs regulate the binding to RHD and shield the NLS of NF- κ B (Karin and Ben-Neriah, 2000). The protein that is best characterised and the first cloned is I κ B α . In spite of the fact that the main function of I κ B α is to bind to NF- κ B proteins to maintain them in the cytoplasm, it is also involved in the removal of NF- κ B from the nucleus (reviewed by Yamamoto and Gaynor, 2004). Free I κ B α has a very short half-life ranging from 70 seconds to less than 1 hour depending on the cell line (Ginn-Pease and Whisler, 1998).

1.6.3 The I κ B kinase (IKK) complex

The IKK complex is a very high molecular weight protein complex composed of several polypeptides (DiDonato *et al*, 1997). It consists of three IKK polypeptides; IKK α (IKK1), IKK β (IKK2), and IKK γ . IKK α and IKK β are catalytic subunits whereas IKK γ is regulatory (reviewed by Karin, 1999). It was revealed that IKK activity is dependent on its phosphorylation and this is achieved by NF- κ B inducing kinase (NIK) (Malinin *et al*, 1997). NIK is a member of the mitogen-activating protein kinase kinase kinase (MAPK3) family which phosphorylates IKK α specifically at Ser-176 (Ling *et al*, 1998).

1.6.3 NF- κ B activation pathways

In most cells NF- κ B is present in a latent state retained in the cytoplasm, sequestered to I κ B α . I κ B α degradation has been observed with all NF- κ B inducers tested (Thanos and Maniatis, 1995). Activation of NF- κ B has been shown with a variety of stimuli including inflammatory cytokines, bacterial products, bacteria, viruses, and oxidative stress (Pahl, 1999). Its activation can be divided into two pathways, the ‘classical’ and the ‘alternative’ pathway (Senftleben *et al*, 2001).

1.6.3.1 The ‘classical’ pathway

After cell stimulation, the IKK complex is activated by the phosphorylation of particular serine residues within the activation loop of IKK α and IKK β (reviewed by Yamamoto and Gaynor, 2004). Then the I κ B protein gets phosphorylated, at Ser 32 and Ser 36 in I κ B α and Ser 19 and Ser 23 in I κ B β (Chen *et al*, 1995 and DiDonato *et al*, 1996), by the IKK complex. This phosphorylation marks the protein for polyubiquitination (Maniatis, 1999 and Sun and Chen, 2004) by an ubiquitin containing complex at two lysines, Lys-21 and Lys-22 (Scherer *et al*, 1995). Roff *et al*, (1996) emphasised the importance of the degradation of I κ B in the activation of NF- κ B, I κ B is then selectively degraded by 26S proteasome. Next the NLS will be exposed and this causes nuclear translocation of NF- κ B to the nucleus. The NF- κ B would then bind to the *cis*-acting κ B sites (5'-GGGPuNNPyPyCC-3') in the DNA to initiate transcription (Pahl, 1999) of the target genes. This pathway is suggested to be involved in the innate immunity whereas the ‘alternative’ pathway is involved in the adaptive immunity (Bonizzi and Karin, 2004).

The involvement of IKK complex in NF- κ B activation does not occur in two cases. One of these is the activation of NF- κ B by short-wavelength ultraviolet C (UVC) light accompanying the degradation of I κ B α . In UVC treated cells, neither IKK activation nor I κ B α phosphorylation was observed (Li and Karin, 1998). The second exception was tyrosine (Tyr-42) phosphorylation of I κ B α (Imbert *et al*, 1996) which was observed during the treatment of cells with tyrosine phosphatase inhibitor (pervanadate), hypoxia (Koong *et al*, 1994), upon reoxygenation of hypoxic cells, or after H₂O₂ treatment (Schoonbroodt *et al*, 2000). This led to the dissociation of I κ B α from NF- κ B. The degradation of I κ B by different pathways is dependent on the cell-type and the kind of stimulus.

Under specific circumstances, such as nutrient deprivation, other proteolytic systems have been implicated such as lysosomal degradation. In Chinese hamster ovary cells, the increase in I κ B degradation has been completely inhibited by lysosomal inhibitors (Cuervo *et al*, 1998) and the half-life of I κ B α pool in the lysosomes has been significantly increased by the presence of antioxidants, suggesting that intracellular ROS mediates I κ B α degradation in the lysosomes. This results in an increase in the NF- κ B activity.

1.6.3.2 The ‘alternative’ pathway

Several years ago an ‘alternative’ pathway leading to NF- κ B activation was reported that occurs specifically in B cells (Senftleben *et al*, 2001 and reviewed in Simmonds and Foxwell, 2008). Unlike the classical pathway, this pathway is dependent only on IKK α , and not IKK β nor IKK γ . RelB/p100 is the target molecule of the IKK α homodimers in this pathway. Following cell stimulation, the IKK α homodimers get phosphorylated at two C-terminal sites. This generates the polyubiquitination and proteasomal degradation of only the inhibitory C-terminal half of p100, and not the whole protein. This would cause the processing of p52 from p100 (see section 1.6.1). Subsequently this would result in the nuclear translocation of RelB/p52 dimer to induce gene expression (reviewed in Yamamoto and Gaynor, 2004).

1.6.4 Redox regulation of NF- κ B

Reduction-oxidation or “Redox” is a term introduced to classify the oxidation and reduction reactions that have occurred. Oxidation is the loss of electrons while reduction is the gain of electrons (Langrehr, 1971). The intracellular redox within the cells is pivotal for various biological events to occur i.e. enzyme activation, DNA synthesis, cell cycle regulation, and transcriptional activation of several genes (Arrigo, 1999). Recently, much interest has been seen with regard to the redox regulation of transcription factors, including NF- κ B.

Glutathione acts as a homeostatic redox buffer (see section 1.4.1.1). It was reported that partial depletion of intracellular glutathione in human T cell line inhibits activation and nuclear translocation of NF- κ B whereas the administration of extracellular cysteine inhibits the DNA-binding activity of the NF- κ B complex. This inhibition is suggested to be caused by the elevation of GSSG levels (Mihm *et al*, 1995). Therefore, it was proposed that GSSG was necessary for NF- κ B activation in the cytoplasm, while GSH was required for the NF- κ B DNA binding (Droge *et al*, 1994). Treatment of human promonocytic (U937) cells with BSO significantly decreased GSH, increased ROS production and activated NF- κ B as a survival cell response against oxidative stress (Filomeni *et al*, 2005).

In addition to these observations, TRx overexpression in the cytoplasm suppresses the degradation of I κ B α (Hirota *et al*, 1999). Therefore an oxidizing

environment is required in the cytoplasm for the activation of NF- κ B (Ginn-Pease and Whisler, 1998). On the other hand a reducing environment was shown to be necessary in the nucleus. The reduction of the cysteine residue at position 62 (Cys-62) in the NF- κ B is essential for its DNA binding. This is thought to be achieved by TRx which regulates the NF- κ B binding by reducing Cys-62 (Matthews *et al*, 1992). It was also demonstrated that TRx translocates from the cytoplasm to the nucleus in response to UVB radiation and TNF- α (Hirota *et al*, 1999), which are both stimuli of NF- κ B activation. It is important to mention that the oxidation of Cys-62 resulted in the inhibition of DNA binding (Arrigo, 1999).

1.6.5 Oxidative stress and NF- κ B activation

NF- κ B was the first transcription factor shown to be regulated by oxidative stress. Several lines of evidence support this hypothesis. The majority of the agents that induce NF- κ B activity may be involved in ROS synthesis (Schreck *et al*, 1991). Furthermore, NF- κ B activation has been shown to be induced directly by ROS i.e. H₂O₂ and by SOD overexpression, and interestingly was prevented by catalase overexpression (Schmidt *et al*, 1995). Finally, antioxidants were shown to be effective in the blockage of NF- κ B activation (reviewed in Schreck *et al*, 1992).

The I κ B α phosphorylation and degradation was shown to be responsive to oxidative stress and blocked by antioxidants (Li and Karin, 1999). It was proposed that ROS generated would induce NF- κ B activation by activating IKK which consequently leads to the dissociation of I κ B α (Sen *et al*, 2004). In several cell lines NF- κ B activation was induced by ROS in the form of H₂O₂ (Byun *et al*, 2002 and Li and Karin, 1999). UVC (200 – 290 nm), UVB (290 – 320 nm), and for the first time UVA (320 – 380 nm) via oxidative stress was able to activate NF- κ B in human skin fibroblasts (Vile *et al*, 1995). Labile-iron release by UVA was found to be a key regulator of UVA-induced NF- κ B activation (Reelfs *et al*, 2004). Specific membrane antioxidants (butylated hydroxytoluene and α -tocopherol) that inhibit lipid peroxidation, have inhibited UVA radiation-dependent activation of NF- κ B. Antioxidants may act to prevent I κ B α phosphorylation and degradation by (i) scavenging radicals, (ii) chelating metal ions to prevent Fenton reaction (see section 1.3.3), (iii) maintaining the activity of other antioxidative enzymes, or (iv) inhibiting the activity of oxidising enzymes (Schreck and Baeuerle, 1992). However it was proven that a number of other cell lines were not sensitive to H₂O₂ treatment,

including monocytic cells, astrocytoma, standard Jurkats except at high concentration, J. Jhan lymphoblastoid T cells, and some other cell lines (Bowie and O'Neill, 2000). Interestingly Lahdenpohja *et al* (1998) have reported that the ROS-forming capacity is weaker after chronic oxidative stress to Jurkat cell lines, and subsequently this has lead to the decreased NF- κ B transcription since I κ B α is not effectively phosphorylated and degraded.

1.6.6 NF- κ B and rheumatoid arthritis

NF- κ B has been proposed to have a central role in inflammation (Tak and Firestein, 2001). Several studies have shown the link between the activation of NF- κ B and a number of inflammatory diseases. Indeed, the NF- κ B complex was found to be highly activated in patients with chronic inflammatory conditions such as rheumatoid arthritis (Handel *et al*, 1995; Asahara *et al*, 1995; Marok *et al*, 1996; Gilston *et al*, 1997 and Han *et al*, 1998). It was also markedly increased in murine collagen-induced arthritis (CIA) (Han *et al*, 1998), and in adjuvant arthritis in rats and in carrageenan rat air pouch model of inflammation (Ellis *et al*, 2000). It is not surprising to know that target genes for NF- κ B include many genes that are involved in the inflammatory response, such as IL-1, TNF- α , IL-6, and inducible nitric oxide synthase (Baeuerle and Henkel, 1994).

The activation of NF- κ B protected animal models of RA against apoptosis and provided a potential link between inflammation and hyperplasia (Miagkov *et al*, 1998). Inhibition of NF- κ B in T cells resulted in reducing the NF- κ B regulated gene expression (Gerlag *et al*, 2000) and decreasing CIA (Seethraman *et al*, 1999 and Gerlag *et al*, 2000). IMD-0506, an inhibitor of IKK, suppressed the nuclear translocation of NF- κ B and the phosphorylation of I κ B α induced by TNF- α in fibroblast-like synoviocytes (Okazaki *et al*, 2005). This also suppressed the production of inflammatory cytokines. Spontaneous production of TNF- α and other pro-inflammatory cytokines is NF- κ B dependent in rheumatoid synovial tissue (Bondeson *et al*, 1999). Treatment with dexamethasone resulted in reducing the number of cells stained for activated NF- κ B in carrageenan rat air pouch model of inflammation (Ellis *et al*, 2000).

Several drugs that are used for treating RA are either inhibitors of NF- κ B activation (e.g. sulfasalazine and gold compounds), or they block I κ B kinase (e.g. aspirin and sodium salicylate), or they increase I κ B α (e.g. glucocorticoids) (Jue *et al*,

1999). Therefore several papers have proposed that the blockage of NF- κ B activation would be a good therapeutic target for both acute and chronic inflammation (Lee *et al*, 1998; Epinat and Gilmore, 1999; Feldmann *et al*, 2002; Wang *et al*, 2006; Tergaonkar, 2006). However, because of its central role in many normal biological processes, global inhibition may not be therapeutically viable (Aya *et al*, 2005). Indeed, inhibition of the NF- κ B activation can result in exacerbation of inflammation if TNF- α production by macrophages is not controlled (reviewed in Simmonds and Foxwell, 2008).

1.6.7 The role of iron in NF- κ B activation

In synovial cells, the NF- κ B is activated and this activation was correlated with increased IRP activity (Guillén *et al*, 1998). The addition of iron in the lungs of rat demonstrated Ft induction, oxidative stress, elevated IL-1 levels, as well as NF- κ B activation (Zhou *et al*, 2003). Immediate labile-iron release by UVA is a key regulator of UVA-induced NF- κ B activation in human skin fibroblasts (Reelfs *et al*, 2004). Studies using liver macrophages and rat brain microglia in cell culture have provided evidence to support the direct participation of chelatable iron in NF- κ B activation and its prevention with iron chelators such as DFO (Youdim *et al*, 1999). Increase in the intracellular labile iron leads to IKK and NF- κ B activation in response to LPS or TNF- α in macrophages, and iron chelators abrogated this response (Xiong *et al*, 2003). It was therefore proposed that iron is responsible for the NF- κ B activation in hepatic macrophages (Xiong *et al*, 2004). Ferritin (heavy chain) was shown to be rapidly induced by NF- κ B activation, which had an antiapoptotic activity, in response to TNF- α treatment (Pham *et al*, 2004). This induction suppressed the accumulation of ROS which is achieved through iron sequestration. This study suggests that H-Ft to be an essential mediator of antioxidant and protective activities of NF- κ B. Recently, Tacchini *et al*, (2008) have demonstrated that the upregulation of NF- κ B by inflammatory signals induces a rapid activation of the transcription factor hypoxia-inducible factor 1 (HIF-1)-dependent TfR1 expression and iron uptake in macrophages.

1.7 Aims and objectives of the project

The synovial fluid and tissue of patients suffering from RA contain high levels of free ‘labile’ iron but its origin has not been properly investigated. Furthermore because of the phenomenon of ischemia-reperfusion, synovial cells’ components are chronically exposed to ROS. We therefore sought to investigate the mechanism underlying the adaptation of synovial T cells to H₂O₂ by evaluating changes in antioxidant molecules and enzymes, intracellular labile iron, and NF-κB activation. Several studies have also shown a role for iron in the progression of inflammatory diseases such as RA (see section 1.2.4 and 1.2.5); but none, to our knowledge, had differentiated between the role of iron in both acute and chronic phases of the disease. Therefore, to investigate the role of iron in both acute and chronic oxidative conditions was necessary.

To achieve our aims, we have extensively studied two cell lines which were Jurkat cells, human T-cell leukaemia cell line. One of them was the parental cell line (J16 cell line) and the other was derived from the parental cell line and gradually adapted to be resistant to H₂O₂ (HJ16 cell line). In established RA, T cells represent the most abundant inflammatory cells in the joint (Aya *et al*, 2005 and Deng and Lenardo, 2006). Experimental and clinical evidence for T cell involvement in the pathology of RA is compelling. Indeed, activated synovial T cells are key initiators and orchestrators of inflammation in RA, and therefore they represent key cellular targets for therapy (Cope *et al*, 2007). Jurkat cells are widely used in the study of T-cell activation processes (Schreck *et al*, 1991) and they are considered as critical determinants of the extent and chronicity of an inflammatory response. The Jurkat T cell lines composed of ‘parental J16’ and ‘H₂O₂ resistant HJ16’ provide a good model to study the differential response of cells to both acute and chronic exposure. We have used the parental cell line to mimic the acute condition after relevant treatments of H₂O₂ and the resistant cell line to mimic the chronic condition. The HJ16 cell line that was established following the gradual adaptation of the J16 cell line to increasing concentrations of oxidising agent H₂O₂, provides us with a useful model to mimic the chronic exposure of T cells in synovium to ROS that is almost certainly involved in the pathology of RA.

We used H₂O₂ as an oxidising agent, since this is commonly used to study the effect of ROS in biochemical pathways. Furthermore it is likely that H₂O₂ is produced in the synovial membrane during the ischemia-reperfusion cycles. Tissues,

in different pathological conditions, are confronted with elevated H_2O_2 concentrations derived either extra- or intracellularly. Hydrogen peroxide is generated during normal metabolism and produced in large amounts by phagocytic cells during inflammation (Hampton and Orrenius, 1997). Because it is uncharged and soluble in both aqueous and lipid phases, H_2O_2 would be expected to distribute rapidly between cellular compartments (Hyslop *et al*, 1995).

In addition to UVA (Morliere *et al*, 1997 and Pourzand *et al*, 1999) and visible light irradiation (Ohishi *et al*, 2005), it has already been shown that the exposure of cells to H_2O_2 (see section 1.3.6) provokes an increase in the LIP that correlates with cell damage and necrotic cell death, although the mechanisms involved has not yet been fully understood. To understand this phenomenon, we have investigated the role of LIP, Ft, and HO (i.e. HO-1 and HO-2) in our cell model. The lysosomal compartment seems to contain the major important cellular pool of labile iron (Petrat *et al*, 2001 and Persson *et al*, 2003) since the degradation of many macromolecules that are rich in iron (e.g. ferritin and mitochondrial electron-transport complexes) occurs in the lysosomes (Radisky and Kaplan, 1998 and Kurz *et al*, 2007) making these organelles vulnerable to oxidative stress (Persson *et al*, 2005). Therefore, understanding the link between lysosomal membrane damage and the above parameters may define pathological mechanisms associated with oxidative stress and lysosomal activity.

The potentially harmful free ‘labile’ iron is recognised as an important promoter of oxidative stress through aiding the production of ROS and thus a potential mediator of the inflammatory process in RA. Previous studies carried out by A. Yiakouvaki in this laboratory (PhD Thesis, 2003 – University of Bath) have provided us with a link between the amount of H_2O_2 -induced labile iron release and the extent of oxidative damage and cell death in Jurkat T cells. Furthermore, the study has shown that adaptation of Jurkat T cells to H_2O_2 can influence the basal level of antioxidant enzymes that is likely to contribute to the resistance of the HJ16 cells to H_2O_2 insult. This thesis has continued the study of Yiakouvaki (2003) by further characterising the differential response of parental J16 and H_2O_2 -adapted/resistant HJ16 Jurkat T cells to H_2O_2 insult with special focus on (1) The role of antioxidant systems (e.g. GSH/GSSG, HO, and Ft); (2) The role of NF- κ B activation; (3) The role of iron; and (4) The role of lysosomes.

In addition to the Jurkat cells, we have performed preliminary studies on a

series of primary human and rat fibroblasts. The human fibroblasts were developed and cultured in our laboratory from human synovial tissues; normal (HN-1), rheumatoid arthritic (HRA-1) and osteoarthritic patients (HOA-1). In addition to the human cells, two primary rat synoviocytes were kindly provided by Dr. Vivienne Winrow (School for Health, University of Bath, UK) for the purpose of our study. The latter were isolated from normal Wistar rats (VW-1) and Wistar rats with adjuvant arthritis (AAVW-1). To gain insight into levels of synovial intracellular iron levels, the labile plasma iron was also measured on a series of normal, RA and OA synovial fluid.

CHAPTER TWO

MATERIALS AND METHODS

2.1 Chemicals and Reagents

Cell culture materials were obtained from Gibco (Germany) except for fetal bovine serum (PAA Laboratories, Austria) and RPMI-1640 medium (Promocell, Germany). All chemicals were from Sigma-Aldrich Chemical (Poole, UK) unless otherwise indicated. Protease inhibitors cocktail tablets, Annexin-V-FLUOS, Klenow enzyme, and Bovine Serum Albumin (BSA) were supplied from Roche (Mannheim, Germany). Glutathione reductase, Hydrogen peroxide solution, and Mowiol[®] 4-88 were obtained from Calbiochem (CN Biosciences LTD, Nottingham). Dimethyl sulphoxide and Nonident P-40 was purchased from VWR International Ltd (Leicestershire, England). Antibodies for immunocytochemistry (p65, Cathepsin-B and Oct-1) were purchased from Santa Cruz Biotechnology, Inc. (Santa Cruz, California). CA-AM (Calcein-acetoxymethyl ester) and LysoSensor[™] Green DND-153 were purchased from Molecular Probes (Leiden, Netherlands). Desferrioxamine mesylate Ph. Eur. (DFO) was purchased from Ciba-Geigy laboratories (Basel, Switzerland). [$\alpha^{32}\text{P}$]-dATP was obtained from Amersham Biosciences UK Limited (Buckinghamshire, England). Stock solutions (100 mM) of deoxynucleotide triphosphates (dNTPs) such as dCTP, dGTP, and dTTP were purchased from Promega (Madison, USA).

2.2 Cell Culture

The Jurkat J16 cells are a human T-cell leukaemia cell line. The HJ16 cells are a polyclonal H_2O_2 resistant cell line which were derived from the J16 cell line after gradual adaptation to 3mM H_2O_2 . In this process, HJ16 cells were treated with increasing concentration of H_2O_2 (i.e. from 0.1 mM to 3 mM) at weekly to fortnightly intervals. After each treatment the surviving cells were allowed to recover normal growth characteristics before further exposure to a higher concentration of

H₂O₂. Following this adaptation, stocks of HJ16 cells were stored in Liquid Nitrogen to ensure their resistance to H₂O₂. The J16 and HJ16 cell lines were kindly provided by Dr. N.D Hall (Pharmacy and Pharmacology, University of Bath, UK). Since in an independent study from our laboratory (i.e. Yiakouvaki, 2003) it was found that HJ16 cells had 3.4-fold higher cell volume than J16 cells (i.e. J16 cells: 0.47 ± 0.08 pl and HJ16: 1.6 ± 0.19 pl), where applicable, normalisation of the data in this thesis was always performed to protein concentration and not to the cell number/cell volume.

Both cell lines were cultured routinely in RPMI-1640 medium supplemented with 10% v/v heat inactivated fetal bovine serum (FBS), L-Glutamine (2 mM), Penicillin/Streptomycin (50 IU/ml each) and 2.7% v/v sodium bicarbonate. They were incubated at 37°C in a humidified atmosphere with 5% CO₂.

2.3 Treatments

2.3.1 Hydrogen peroxide (H₂O₂) treatment

Stock solution: 176mM in phosphate buffered saline (PBS)

Hydrogen peroxide (H₂O₂) solutions were freshly prepared from a 30% stock solution. Treatments were performed in serum free media (SFM) to prevent the degradation of H₂O₂ by the catalase present in the serum. Cells were incubated with the relevant concentration of H₂O₂ for 30 minutes. After centrifugation, they were resuspended and incubated in the conditioned media for the times indicated in the Results section (see Chapter Three). The J16 and HJ16 cell lines were both tested routinely during the experimental work to demonstrate their differential sensitivity to H₂O₂ treatment.

2.3.2 Buthionine-[S,R]sulfoximine (BSO) treatment

Stock solution: 50mM in phosphate buffered saline (PBS)

Unless otherwise stated, cells were incubated with 25 µM BSO for 18 h at 37°C in the conditioned media prior to experimentation.

2.3.3 DFO treatment

Stock solution: 150 mM in H₂O

Unless otherwise stated, cells were treated with 100 μ M of DFO for 18 h at 37°C prior to experimentation.

2.3.4 Hemin treatment

Stock solution: 20 mM in dimethyl sulphoxide.

Unless otherwise stated, cells were treated with 20 μ M of hemin for 18 h at 37°C prior to experimentation.

2.4 MTT Assay

The MTT assay is widely used in cell proliferation and cytotoxicity assays (Berridge *et al*, 1996). It is a sensitive colorimetric assay (Mosmann, 1983 and Doyle and Griffiths, 1998) that was performed to determine the viability of cells after relevant treatments. Cellular and mitochondrial dehydrogenase enzyme converts MTT [3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyl tetrazolium bromide], a yellow water-soluble substrate, into a dark blue formazan product that is insoluble in water. The amount of formazan produced is directly proportional to the viable cell number.

The MTT stock solution of 5mg/ml in PBS was filtered through a 0.2 μ m filter (Ministart[®], Germany) for sterilisation and stored at –20°C. On the day of the experiment and after the relevant treatments, the pellets were resuspended in SFM containing MTT stock solution at a final concentration of 0.5mg/ml. From this solution, 100-200 μ l were placed, in triplicate, into a 96 well microplate. The 96-well microplate was then incubated for 3h at 37°C. Then the MTT / SFM solution was aspirated and 50-200 μ l of dimethyl sulphoxide (DMSO) was added to each well. Finally, the plate was swirled for 3 minutes by a 3D rocking platform (Stuart Scientific, UK) and the absorbance was read by VERSAmax[™] (Molecular devices, California) at 550 nm.

2.5 Flow Cytometric Analysis

Quantification of apoptotic, necrotic, and live cells were evaluated by flow cytometry. Apoptotic lymphocytes were shown to express phosphatidylserine (PS) on the outer layer of the plasma membrane (Fadok *et al*, 1992). In the early stages of apoptosis, PS translocates from the inner part of the plasma membrane to the outer layer. Annexin-V-FLUOS is a phospholipid binding protein with a high affinity for PS. Therefore it is suitable for the detection of apoptotic cells. On the other hand, necrotic cells that lose cell membrane integrity are stained with both Annexin-V-FLUOS and Propidium Iodide (PI). Therefore, Annexin-V-FLUOS and PI double-staining can differentiate between necrotic and apoptotic cells.

After relevant treatments and incubation periods, cells were collected and washed with PBS. Cells were then resuspended in 100 µl of incubation buffer (10 mM Hepes/NaOH pH 7.4, 140 mM NaCl, 5 mM CaCl₂) containing Annexin-V-FLUOS (20µl/ml) and PI (20µl/ml). Samples were then transferred to a 5ml polystyrene round-bottom tube and incubated for 10-15 minutes at room temperature (RT) in a dark place. Data analysis was performed using CellQuest software (Becton-Dickinson, Erembodegem, Belgium).

2.6 Protein Measurements

Protein concentrations were measured according to the method of Bradford (1976) with slight modification. This modification was performed to enable the measurements of the protein content to be carried out in the 96-well plate to decrease the amount of protein extract used. To calibrate the standard curve, bovine serum albumin (BSA, 2 mg/ml) was first diluted (1:1) with MilliQ water (i.e. to 1 mg/ml) and used at final concentrations of 0, 1, 2, 4, 6, 10, 15, and 20 mg/ml. The total volume of cellular extract (1-5 µl) or BSA (0-20 µl) with MilliQ water used in the each well was 160 µl, done in duplicates. 40 µl of Bio-rad Protein Reagent (Bio-rad, 500-0006) was finally added, and the solution was thoroughly mixed with a pipette (preferably, a multichannel pipette). The absorbance was read by VERSAmaxTM (Molecular devices, California) at 595 nm filter.

2.7 Glutathione Measurements

Total intracellular glutathione was measured according to the spectrophotometric method developed by Tietze (1969). It is an enzymatic recycling procedure which offers a high sensitivity rate. Glutathione is assayed by a system in which it is readily oxidised by 5,5'-dithiobis(2-nitrobenzoic acid) DTNB and reduced by NADPH in the presence of glutathione reductase (GR). The rate of 2-nitro-5-thiobenzoic acid formation is monitored and the glutathione is determined by the comparison of the result with a standard curve with the known amounts of glutathione (Griffith, 1980 and Pourzand *et al*, 2000).

The standard curve consists of GSSG stock solution diluted in [5% TCA in 2 mM EDTA] in a range of 0.01 – 2 μ M. Cells (1.0×10^6) were incubated with BSO for 18 h (see section 2.3.2). After the incubation period, the pellets were resuspended in cold PBS and then extracted in a freshly prepared mixture of [5% TCA in 2 mM EDTA] in order to give 500 μ L per 1.0×10^6 of cells.

100 μ L samples from either the stock solution (0.01 – 2 μ M) or the treated cells were transferred to an eppendorf tube containing 1ml of phosphate buffer, 50 μ L of NADPH (5 mM in 0.5% NaHCO_3), and 20 μ L of freshly prepared DTNB (1.5 mg/ml in 0.5% NaHCO_3). The eppendorf tube was then placed in a 25°C water bath for 10 minutes. Next, 100 μ L of GR (18 u/ml in phosphate buffer) was added to the mixture and change in absorbance was monitored by a Uvikon 922 spectrophotometer (Kontron instruments, Italy) for 6 minutes at 412 nm (25°C).

The total intracellular glutathione was then normalised by two determinations, cell count and total cellular protein. For this purpose, either the viability of cells were assessed using a haemocytometer and the cells were stained by Trypan blue (Doyle and Griffiths, 1998), or the cells were lysed and the total cellular protein was then measured via the Bradford assay (see section 2.6).

2.8 Electrophoretic Mobility Shift Assay (EMSA)

An adaptation of the protocol described by Schreiber *et al*, (1989) was used for the analysis of the activation of NF- κ B by EMSA. Typically, 0.5×10^6 cells from four 6 cm plates of specified treatments were used. Cells were then washed with 2ml ice-cold PBS and pelleted by centrifugation at 1500 rpm (400 xg, Falcon 6/300 -

MSE) at 4°C. The pellet was resuspended with 80 µl of Buffer A [10 mM HEPES (pH 7.9), 10 mM KCl, 0.1 mM EDTA, 0.1 mM EGTA] with a fresh supplementation of DTT (1 mM) and Protease inhibitors cocktail tablets (20x), and allowed to swell for 15 minutes on ice. 0.5% of 10% w/v NP-40 was added and the eppendorf was vigorously vortexed for 10 seconds. The lysates were then centrifuged for 30 seconds at 13,000 rpm (9000 xg, Micro Centaur – MSE). The supernatant which contained the cytoplasmic proteins was collected and flash-frozen on dry-ice. It was stored at -80°C. The nuclear pellet was then resuspended in buffer C [20 mM HEPES (pH 7.9), 0.4 M NaCl, 1 mM EDTA, 1 mM EGTA] with a fresh supplementation of DTT (1 mM) and Protease inhibitors cocktail tablets (20x). The Eppendorf was vigorously rocked for 15 minutes at 4°C on a shaking platform. The nuclear extract was then centrifuged for 5 minutes at 13,000 rpm (9000 xg) in a Biofuge 13 centrifuge (Heraeus Instruments) in a cold room (4°C). The supernatant (nuclear proteins) was collected and flash-frozen on dry-ice. It was stored at -80°C. Protein concentration was measured (see section 2.6) in duplicates on 3 µl aliquots of the extracts and the mean was taken.

2.8.1 Annealing and purification of the oligonucleotides

The annealing and purification of the oligonucleotides were kindly developed and performed by Dr. Olivier Reelfs through the following protocol:

The oligonucleotides possess *HindIII* and *SalI* linker sites on their 5' and 3' end, respectively (Zabel *et al*, 1991). The sequence of the “κB” oligonucleotides used as a radioactive DNA was as follows:

5'- AGCTTCAGAGGGGACTTTCCGAGAGG - 3'

3' – AGTCTCCCCTGAAAGGCTCTCCAGCT – 5'

Equal amounts of each oligonucleotide and its complementary strand were mixed in a buffer containing 100 mM Tris (pH 7.6), 100 mM MgCl₂, boiled for 3 minutes and the mixture was left to be cooled at RT. Proper annealing was first verified on a 20% polyacrylamide gel, and then purified on a 20% polyacrylamide preparative gel in a 0.5x TBE buffer [44.4 mM Tris, 44.4 mM borate, 1 mM EDTA (pH 8.0)]. Elution of the band from the gel was performed by electroelution (Biotrap; Schleicher & Schuell, Switzerland), the oligonucleotides were ethanol precipitated, resuspended in TE buffer [10 mM Tris (pH 7.6), 1 mM EDTA (pH 8.0)] and aliquoted at -20°C.

2.8.2 Preparation of the probe

100 ng of the annealed oligonucleotide was labelled by end-filling using the Klenow enzyme in the presence of 50 μ Ci [α^{32} P]-dATP, 0.033 mM of cold dCTP, dGTP, dTTP, and 3 μ l of 10x polymerase buffer [0.5 M Tris (pH 7.5), 0.1 M MgCl₂, 10mM DTT, 0.5 mg/ml BSA].

2.8.3 Binding reactions

For detecting NF- κ B binding activity after relevant treatments of both J16 and HJ16 cell lines: First, 6 μ g of the nuclear extract was incubated for 10 minutes at RT in a freshly prepared buffer composed of 20 mM HEPES (pH 7.9), 12% glycerol, 0.2 mM EDTA, 0.2 mM PMSF, 0.5 mM DTT, 5 mM MgCl₂, 3mM ATP, and 100 μ g poly [(dI)-(dC)]. Salt concentration was adjusted to 100 mM in each sample. After the 10 minutes incubation period, 0.3 ng of the labelled oligonucleotide was added to the mixture and incubated for 30 minutes at RT.

2.8.4 Running and processing the gel

The reaction mixtures were loaded on a 5 % polyacrylamide gel and electrophoresed at 140V in 0.4x TBE buffer at RT for 2-3 h. Next the gel was fixed in a mixture of methanol: acetic acid: water (at proportions of 10: 10: 80) for 20-30 minutes and then it was vacuum-dried for 1.5 h (in high mode). Results were shown as autoradiograms using high performance chemiluminescence films (Amersham Biosciences UK Limited, England) developed by Fuji X-ray Film Processor (Fuji Photo Film Co, Japan). The bands were scanned and the quantification was assessed using LabImage software - Version 2.7.2 (Kapelan Bio-Imaging Solutions, Germany).

2.9 **Western blot analysis**

Whole cell extracts were prepared by the lysis of the cells with 0.1% Triton X-100 lysis buffer [20mM TrisHCl (pH 8), 0.1% Triton X-100, 10% glycerol, 2mM EDTA, 137mM NaCl, 100mM PMSF, Protease inhibitors cocktail (20x)]. Protein measurements were then determined by Bradford's assay (see section 2.6). Equal amounts of protein (40 μ g) were diluted with 4x loading buffer [180 mM Tris (pH

6.8), 3% SDS, 150 mM DTT, 30% glycerol, 0.0015% bromophenol blue, 0.53 ml Milli Q water] and then boiled for 5 minutes at 95°C. They were then resolved by Polyacrylamide (10% acrylamide) gel electrophoresis (SDS-PAGE) for ~ 1.75 h at 150 volts (V) in running buffer (1.5 % w/v Tris, 7.2 % w/v glycine, 0.5 % SDS) and transferred to nitrocellulose membranes (Amersham Biosciences, UK) at 4°C or 1.5 h at 100 V in a transfer buffer (3% w/v Tris, 14.4 % w/v glycine, 20 % v/v methanol). The transfer was verified by the colouration of the membrane with Ponceau S solution for 1-2 minutes and then rinsed several times with a small amount of Milli Q water to reveal the bands. The membrane was then thoroughly washed with 0.5% Tween-20 (Acros Organics, Belgium) PBS (PBST) and blocked for 1 h in 5% w/v milk powder in 0.05% PBST, placed on a rocking platform (Stuart Scientific, UK). Next, the membrane was washed once with 0.5% PBST and incubated with one of the following primary antibodies in 5% w/v milk in 0.05% PBST overnight at 4°C with; 1:50 anti-HO-1 mouse monoclonal antibody (OSA-110, Stressgen Bioreagents), 1:200 anti-HO-2 rabbit polyclonal antibody (kindly provided by Prof. Rex Tyrrell, University of Bath), or 1:500 anti-actin mouse monoclonal antibody (Sigma, A4700). The membrane was then washed extensively with 0.5% PBST and incubated with (1:500 for HO-1 and 1:2000 for Actin) goat anti-mouse IgG peroxidase conjugated (Sigma, A4416) or (1:1500 for HO-2) anti-rabbit IgG (whole molecule)-Peroxidase (Sigma, A6154) in 5% w/v milk in 0.05% PBST for 1 h at RT on a rocking platform (Stuart Scientific, UK). The membrane was then washed extensively with 0.5% PBST, and the protein bands were finally detected using enhanced chemiluminescence (ECL) plus detection system according to manufacturer's instructions (Amersham Biosciences). *Re-blot Plus* (Strong Antibody Stripping Solution) was used in order to re-blot, according to manufacturer's instructions (Chemicon, 2504).

2.10 Ferritin ELISA

Enzyme-Linked ImmunoSorbent Assay (ELISA) is a biochemical technique used mainly in immunology to quantify the presence of an antibody or an antigen in a sample. Reagents for ferritin ELISA were kindly provided by Dr. Santambrogio (Milan, Italy), and the assay performed as described in Santambrogio *et al*, 2000 and 2007. Cytosolic ferritin concentrations were determined in cell lysates by

monoclonal antibodies specific for human H- and L- ferritin subunits (rH02, LF03), and mitochondrial ferritin concentrations in mitochondria enriched fractions by mouse polyclonal antibody specific for mitochondrial ferritin (Moc α HuFtMt) by the means of ELISA, then normalised to protein concentration (see section 2.6).

For cell lysates: After relevant treatments, cells (10×10^6 cells / condition) were washed with ice cold PBS and the lysates were prepared as described in 2.9. The supernatant was then flash frozen on dry ice with ethanol and kept at -80°C until use. Microtiter plates were coated with 0.1 ml of $10\mu\text{g/ml}$ of rH02 or LF03 antibodies diluted in 50 mM Na carbonate buffer pH 9.5. Standard ferritins and samples were diluted in PBST with 1% BSA (0.05% Tween-20 in PBS-BSA) and 0.1 ml was added to the plates, incubated for 1 h at 37°C , washed three times with PBST (0.05% Tween-20 in PBS), and further incubated for 1 h at 37°C with the same HRP-labelled antibodies (LF03-HRP 1:3000 and rH02-HRP 1:15,000, in PBST + 1% BSA) to reveal the bound ferritin. The peroxidase activity was developed with *o*-phenylenediamine dihydrochloride (Sigma, P1526).

For mitochondria preparation (Smith, 1967 and Atorino *et al*, 2003) : After relevant treatments, cells (10×10^6 cells / condition) were washed with ice cold PBS and resuspended in ice cold-isotonic buffer (250 mM Sucrose, 5 mM tris-HCl pH 7.5, 0.1 mM PMSF) and homogenised using PowerGen 125 Homogenizer (Fisher Scientific, UK) for 30 seconds. This was then centrifuged at 600 xg for 15 minutes at 4°C in a Biofuge 13 centrifuge (Heraeus Instruments) to remove the nuclei and cell debris. Next, the supernatant was collected and centrifuged at 13,000 rpm (9000 xg) in a Biofuge 13 centrifuge (Heraeus Instruments) for 25 minutes at 4°C . The pellet was finally dissolved in the same buffer containing 1mM EDTA and centrifuged at 13,000 rpm (9000 xg) for 25 minutes at 4°C in a Biofuge 13 centrifuge (Heraeus Instruments). The mitochondrial pellet was flash frozen on dry ice with ethanol, and kept at -80°C until use. On the day of the assay, the pellet was resuspended in the ice cold-isotonic buffer. As above, microtiter plates were coated with 0.1 ml of $10\mu\text{g/ml}$ of Moc α HuFtMt antibodies diluted in 50 mM Na carbonate buffer pH 9.5. Standard ferritins and samples were diluted in PBST with 1% BSA (0.05% Tween-20 in PBS-BSA) and 0.1 ml was added to the plates, incubated for 1 h at 37°C , washed three times with PBST (0.05% Tween-20 in PBS), and further incubated for 1 h at 37°C with the same HRP-labelled antibody (Moc α HuFtMt-HRP 1:6000, in PBST + 1%

BSA) to reveal the bound ferritin. The peroxidase activity was developed with *o*-phenylenediamine dihydrochloride (Sigma, P1526).

2.11 Neutral red uptake assay

The neutral red (NR) uptake assay is a cell survival/viability assay, based on the ability of the viable cells to incorporate and bind NR. Neutral red is a relatively non-toxic, weakly cationic dye which was introduced as a vital stain in 1894 (Dietz *et al*, 1979). This dye enters the cells and accumulates in the lysosomes (since it has a low pH) and binds to its matrix by non-ionic diffusion, a mechanism by which weak acids and bases pass through lipid membranes in a non-ionised form (Anderson and Orci, 1988).

The neutral red stock solution was made by thoroughly dissolving 0.02g of NR powder in 5ml of Milli Q water. 500 µL of the stock solution was added to 39.5 ml of 10 % FCS-RPMI, this solution was stored overnight at 37°C to remove fine precipitates and dye crystals which form when NR is mixed with the medium (Borenfreund and Puerner, 1985). On the day of the assay, this solution was centrifuged for 10 minutes at 1200 rpm (120 xg) in a Jouan B 3.11 centrifuge and filtered through a 0.2 µm filter (Ministart[®], Germany). The cells were centrifuged and washed once with PBS, resuspended in 2-3 ml of the filtered dye/media mixture, and then incubated at 37°C for 1.5 h. Next, they were centrifuged at 1500 rpm (300 xg) in a Falcon 6/300 MSE centrifuge and fixed with 500 µL of the fixing solution (40% formaldehyde + 10% CaCl₂) for a maximum of 1 minute since formaldehyde will result in the extraction of the dye. The cells were centrifuged again and lysed with 500 µL of lysis buffer (1% acetic acid + 50% ethanol). 150 µL of each sample was placed in duplicate in a 96-well plate and the absorbance was measured at 540 nm by VERSAmax[™] (Molecular devices, California).

2.12 Lysosensor immunofluorescence

The LysoSensor[™] Green DND-153 was used to monitor the integrity of the lysosomal membrane after relevant treatments. This probe is a fluorescent pH indicator that partitions into acidic organelles at the result of protonation.

Treatments were performed when cells were placed on sterilised glass coverslips laid on the bottom of 3cm³ plates, done in duplicate. After relevant treatments, 500 µL of methanol (stored in -20°C) was placed on the plates for 5 minutes, to fix the cells on the coverslips. The methanol was then aspirated and the plates were kept at -20°C till use. On that day, 1 ml of PBS was added to the plates for 10 minutes to rehydrate the cells. The PBS was then aspirated and 500 µL of the 1 µM probe (stock) solution (freshly prepared in 10% FCS-RPMI) was placed on the cells and they were then incubated for 2 h at 37°C. Meanwhile, microscope slides were prepared and cleaned by soaking them in ethanol for 5 minutes, then with Milli Q water for 2 minutes and finally in acetone for 5 minutes. After the 2 h, the coverslips were drained, washed gently with PBS, and mounted overnight on the slides containing 20 µL of Mowiol[®] 4-88 mounting medium. Finally, the cells were analysed by LSM 510 Confocal Microscope (Carl Zeiss system, Germany) and the objective used was described as Plan-Apochromat 63 x / 1.40 oil DIC. The line of excitation used from the Argon laser was 488 nm and the emission was passed through a Long Pass 505 nm (LP 505) filter. Pictures were scanned at a resolution of 1024x1024 pixels; this is equivalent to an approximate resolution of 1.05 mega pixels.

2.13 Immunocytochemistry

Treatments were performed when cells were placed on sterilised glass coverslips laid on the bottom of 3cm³ plates, done in duplicate. After relevant treatments, cells were fixed by methanol (stored in -20°C) for 5 minutes. The methanol was then aspirated and the plates were stored in -20°C till use. On that day, 1 ml of PBS was added in the plates for 10-15 minutes to rehydrate the cells. The PBS was aspirated and the non-specific sites were blocked by the addition of 150 µL of Buffer X (0.1 % TritonX100 + 2% BSA in PBS) at room temperature (RT) for 10 minutes. The primary antibodies used were Cathepsin B, NF-κB (p-65), and Oct-1 (C-21). The dilution was 1:100 in Buffer X and they were incubated for 1 h at RT placing parafilm on the top. After the 1 h passed, the cells were gently washed twice with PBS and were then incubated with the secondary antibody (dilution 1:100, in Buffer X) for another 1 h at RT. The secondary antibody used

was a FITC conjugated goat anti-rabbit IgG (Sigma, F9887). Meanwhile, microscope slides were prepared and cleaned by soaking them in ethanol for 5 minutes, then with Milli Q water for 2 minutes and finally in acetone for 5 minutes. After the 1 h incubation time, the coverslips were then drained, gently washed twice with PBS, and mounted overnight on the slides containing 20 μ L of Mowiol® 4-88 mounting medium. Finally, the cells were analysed by LSM 510 Confocal Microscope (Carl Zeiss system, Germany) and the objective used was described as Plan-Apochromat 63 x / 1.40 oil DIC. The line of excitation used from the Argon laser was 488nm and the emission was passed through a Long Pass 505nm (LP 505) filter. Pictures were scanned at a resolution of 1024x1024 pixels; this is equivalent to an approximate resolution of 1.05 mega pixels.

2.14 Preliminary Clinical data

In collaboration with Dr. James Murray orthopaedic consultant (Frenchay and the Avon Orthopaedic Centre in Southmead, Bristol) and according to the South West Local Research Ethics committee approval BA 574 (2003/4), we have received synovial fluid and synovial tissue biopsies from normal, rheumatoid arthritic, and osteoarthritic patients (see table 2.1 for the statistics). The synovial fluid was centrifuged at 3000 rpm (1000 xg) in a Falcon 6/300 MSE centrifuge for 15 minutes to remove debris and any other unwanted particles. The supernatant was collected and stored at -80°C. Before culturing fibroblasts from the biopsies, they were washed with 1ml Penicillin/Streptomycin (50 IU/ml each), they were then placed in 6 cm plates, sliced and sheared into small pieces. The biopsy was maintained in 15% v/v FBS-EMEM supplemented with an antibiotic mix [Penicillin G - 10^7 units (Sigma); Streptomycin sulphate – 10g (Sigma); Fungizone – 100 ml (Gibco)] prepared in our laboratory. The fibroblasts were then cultured and grown in 15% v/v FBS-EMEM supplemented with), L-Glutamine (2 mM), Penicillin/Streptomycin (50 IU/ml each) and 2.7% v/v sodium bicarbonate. They were incubated at 37°C in a humidified atmosphere with 5% CO₂.

In addition to the above, Dr Vivienne Winrow (School for Health, University of Bath) kindly supplied us with primary rat synoviocytes (fibroblasts), labelled VW-1 and adjuvant arthritic (AA) rat fibroblasts, labelled AAVW-1.

Synovial Fluid

Condition	Collected	Stored @ -80°C	Analysed
Normal	1	1	1
RA	6	6	2
OA	23	23	6

Synovial Biopsy

Condition	Collected	Cultured	Analysed
Normal	5	1	1
RA	17	2	1
OA	25	2	1

Table 2.1 :

Table listing the synovial fluid (top) and the synovial knee biopsies (bottom) received and analysed for either labile plasma iron (LPI) or labile iron pool (LIP), respectively.

Adjuvant arthritis is a chronic model and a standard procedure which has been used for many years (Pearson, 1956 ; Currey and Ziff, 1968 ; Andrews *et al*, 1987). It is a useful model for screening putative therapeutics for diseases such as human RA; it induces both soft inflammation and bone destruction (Ragno *et al*, 1996). Rats with AA share many characteristics with human RA such as genetic linkage, synovial CD4⁺, and T cell dependence (Goodson *et al*, 2003). They were grown in 10% v/v FBS DMEM (1000 mg/L glucose; Pyruvate) supplemented with L-Glutamine (2 mM), Penicillin/Streptomycin (50 IU/ml each) and 2.7% v/v sodium bicarbonate (0.27%). They were incubated at 37°C in a humidified atmosphere with 5% CO₂. Since the human and the rat fibroblasts are not cell line (ie not immortalised), they will not passage indefinitely. Therefore, as Dr. Vivienne Winrow advised, functional studies were not performed beyond passage 12 (maximum).

2.15 LIP determination in 96 well-plates

The level of LIP was determined by an adaptation of the method developed by Epsztejn *et al*, 1997 and Petrat *et al*, 1999. The cytochemical calcein-acetoxymethyl ester (CA-AM) assay is well established as a technique for the assay of cellular LIP. The principle of this assay is that non-fluorescent lipophilic CA-AM that easily penetrates cellular membranes produces fluorescent CA when rapidly cleaved by unspecific cytosolic esterases. The fluorescent CA is a fluorochromic alcohol that chelates labile iron (Tenopoulou *et al*, 2007). The level of intracellular CA-Fe complexes was determined by the increase in fluorescence produced by the addition of the fast membrane permeable iron chelator, salicylaldehyde isonicotinoyl hydrazone (SIH). Salicylaldehyde isonicotinoyl hydrazone (kindly provided by Professor Ponka, Lady Davis Institute - Canada) is a lipophilic strong chelator that restores the fluorescence by removing the complexed iron (Glickstein *et al*, 2005).

Cells were grown for 48 h in dark 96-well plates (Costar, 3603) at a density of 6×10^4 cells / well (final density needed $\sim 8 \times 10^4$ cells / well). After the 48 h, the conditioned media was aspirated and the cells were washed once with DPBS (Dulbecco's phosphate buffered saline with Ca and Mg – Cambrex, Belgium). After H₂O₂ treatments, cells were washed once with DPBS and loaded with 0.25 μ M CA-AM in Earle's minimum essential media [containing 20 mM HEPES (pH 7.3) and

BSA 1 mg/ml] for 15 min at 37°C. The cells were then washed with DPBS, and the fixing solution [10 mM HEPES buffer containing 150mM NaCl and 2 mM diethyltriamine-pentaacetic acid (DTPA)] was added. The fluorescence (F1) was then measured (Excitation 485 – Emission 535) by a Fluoroskan Ascents microplate reader (Labsystems, OY). 200 µM of SIH was then added, and the plate was placed on a rocking platform (Stuart Scientific, UK) for 15 minutes to allow chelation. After the 15 minutes, the fluorescence (F2) was measured (Excitation 485nm – Emission 535nm). The fractional increase of fluorescence ($\Delta F = (F2-F1) / F2$) was first determined by the calibration curve and then normalised to total cellular protein. This correlates with the LIP (µM/µg) within the cells (Duarte and Jones, 2007).

The calibration curve was prepared with ferrous ammonium sulphate (Petrat *et al*, 2000). It was initially diluted with DPBS to 1 mM and then to 1µM (final) and from it 1:1 serial dilutions were prepared, till 2.44×10^{-4} µM (total = 12 concentrations were used). 0.25 µM of CA (Sigma, C0875) was added to the 12 serial dilutions and the fluorescence (F1) was measured (Excitation 485 – Emission 535) by a Fluoroskan Ascents microplate reader (Labsystems, OY). 200 µM of SIH was then added to the serial dilutions, and the plate was placed on a rocking platform (Stuart Scientific, UK) for 15 minutes to allow chelation. After the 15 minutes, the fluorescence (F2) was measured (Excitation 485 – Emission 535). For the calibration curve (Darbari *et al*, 2003), the fractional increase of fluorescence ($\Delta F = (F2-F1) / F2$) was plotted against the iron concentration used ($y = 9.981x + 0.088$, is the linear equation of the trendline).

2.16 Labile plasma iron (LPI) measurements

Labile plasma iron (LPI) represents the redox-active and chelatable component of non-transferrin-bound iron (NTBI) (Le Lan *et al*, 2005). It is capable of permeating into organs and inducing tissue iron overload (Cabantchick *et al*, 2005). The method of measuring LPI is based on its capacity to generate reactive oxygen radicals when prompted with ascorbate in a manner blockable by specific iron chelators such as DFO. Non fluorescent dihydrorhodamine (DHR) is converted by various oxidants, such as reactive oxygen radicals, to the fluorescent form.

As described by Esposito *et al*, (2003): Quadruplicates of 20 μL synovial fluid (SF) were placed in a clear-bottom 96 well plate. To two of the four wells, 180 μL iron-free HEPES buffered saline (HBS; HEPES 20mM, 60nM DFO, NaCl 150 mM, pH 7.4 – treated with 1g of 100ml⁻¹ Chelex-100) containing 40 μM ascorbate and 50 μM DHR (= Test mix) was placed. 180 μL iron-free HBS containing 40 μM ascorbate, 50 μM DHR, and 50 μM DFO was added to the other two wells (= Reference mix). The kinetics of the fluorescence was measured with the excitation at 485 nm and the emission at 538 nm by a Fluoroskan Ascents microplate reader (LabSystems, OY). This was measured for 40 minutes, with readings every 2 minutes, immediately after the addition of the test and reference mix. The slopes (r) of DHR fluorescence intensity with time were calculated from measurements taken 15 and 40 minutes. The duplicate values of r in the presence and absence of DFO, r_{DFO} and r , respectively, were averaged, and the LPI concentration (μM) was determined from calibration curves relating the difference in slopes with and without DFO against Fe concentration: $\text{LPI} = \Delta r / r_{\text{st}} = (r - r_{\text{DFO}}) / r_{\text{st}}$.

Calibration curves were obtained by spiking plasmalike medium (PLM) with Fe:NTA, 1:7 (mol/mol), followed by serial dilution in PLM and incubation for 30 minutes at 37°C to allow binding of the Fe. Plasmalike medium (PLM) contained 20 mM HEPES, 150 mM NaCl, 120 μM sodium citrate, 40 μM sodium ascorbate, 1.2 mM sodium phosphate dibasic, 10 mM sodium bicarbonate, and 40 mg/mL human serum albumin (pH 7.4). Fe³⁺/NTA complexes were formed by mixing 70 mM nitrilotriacetic acid (NTA), titrated to pH 7.0 with NaOH, with 20 mM ferrous ammonium sulphate to produce a Fe/NTA molar ratio of 1:7 and allowing the Fe²⁺ to oxidise to Fe³⁺ in ambient air for 30 minutes. Quadruplicates of 20 μL of these samples were assayed for LPI as described in the previous paragraph.

2.17 Statistical analysis of data

Results were expressed as the mean \pm standard deviation. Data were analysed using paired or unpaired Student's one-tailed t -test, as appropriate. The p value of < 0.05 was considered to indicate a significant difference between groups of data.

CHAPTER THREE

RESULTS

Background:

The response of cells to either an acute (single high dose) or chronic (repeated low doses) exposure to oxidising agents is quite different. Depending on the degree of the oxidising insult, acute exposure could trigger a series of intracellular antioxidant defence mechanisms that counteract the damage caused but if these are not sufficient, cells will die by either apoptosis or necrosis. In chronically exposed cells, the antioxidant defence mechanism is altered as exposure of cells to low doses of oxidants usually provokes the development of a distinct adaptive response that differs quite sharply from that following acute exposure. Because of such adaptive responses, cells may withstand high toxic doses of the oxidising agent that would otherwise be lethal. The study of the mechanisms underlying the adaptive responses of cells to oxidising agents provides clues to understand the promotion and progression of the chronic inflammatory process in diseases such as Rheumatoid Arthritis (RA). A potentially major factor influencing this process is that the rheumatoid synovium is relatively hypoxic, and is exposed to chronic cycles of hypoxia and reperfusion. This promotes oxidative stress, which has marked effects on many cell types, including enhanced production of pro-inflammatory cytokines by mononuclear cells.

The Jurkat T cell lines composed of 'parental J16' and 'H₂O₂ resistant HJ16' provide a good model to study the differential response of cells to both acute and chronic exposure. Furthermore the HJ16 cell line that was established following adaptation of J16 cell line to increasing concentrations of oxidising agent H₂O₂, provides us with a useful model to mimic the chronic exposure of T cells in synovium to ROS that are almost certainly involved in the pathology of RA.

The potentially harmful free 'labile' iron is recognised as an important promoter of oxidative stress through aiding the production of ROS and thus a potential mediator

of the inflammatory process in RA. Previous studies carried out by A. Yiakouvaki in this laboratory (PhD Thesis, 2003 – University of Bath) have provided us with a link between the amount of H₂O₂-induced labile iron release and the extent of oxidative damage and cell death in Jurkat T cells. Furthermore the study has shown that adaptation of Jurkat T cells to H₂O₂ can influence the basal level of antioxidant enzymes that is likely to contribute to resistance of HJ16 cells to H₂O₂ insult.

This thesis has continued the study of Yiakouvaki (PhD Thesis, 2003 – University of Bath) by further characterising the differential response of parental J16 and H₂O₂-adapted/resistant HJ16 Jurkat T cells to H₂O₂.

3.1 Determination of the sensitivity of J16 and HJ16 cell lines to H₂O₂

The accumulation of the damage caused by ROS, including H₂O₂, plays an important role in the aetiology and/or progression of a number of diseases (Moskovitz *et al*, 2002). In order to evaluate the cytotoxicity of H₂O₂ on J16 (parental) and HJ16 (H₂O₂-resistant) cell lines, both cell lines were treated with various concentrations of H₂O₂ (i.e. 0.1, 0.5, 1, and 3 mM) and two cytotoxicity assays were performed; MTT (see section 2.4) and flow cytometry (see section 2.5). These assays were performed 24 h following H₂O₂ treatment, since previous studies have revealed that the cytotoxicity of H₂O₂ towards these cell lines is only apparent from 18 h post-treatment time point (A.Yiakouvaki - PhD thesis, 2003). Epsztejn *et al*, (1999) have also reported that cell damage and death was only present 24 h-post H₂O₂ treatment.

3.1.1 MTT assay

According to MTT analysis that assesses cell viability, treatment of both cell lines with H₂O₂ resulted in a concentration-dependent decrease in cell viability (see figure 3.1). However J16 cells were more sensitive to H₂O₂ treatment than HJ16 cells. Indeed even a concentration of H₂O₂ as low as 0.1 mM was able to cause damage to the J16 cells as the intracellular dehydrogenase activity of H₂O₂-treated cells decreased to 57.4 ± 0.8 % of the control. On the other hand, the HJ16 cells were clearly resistant to H₂O₂ treatment up to 3 mM final concentration.

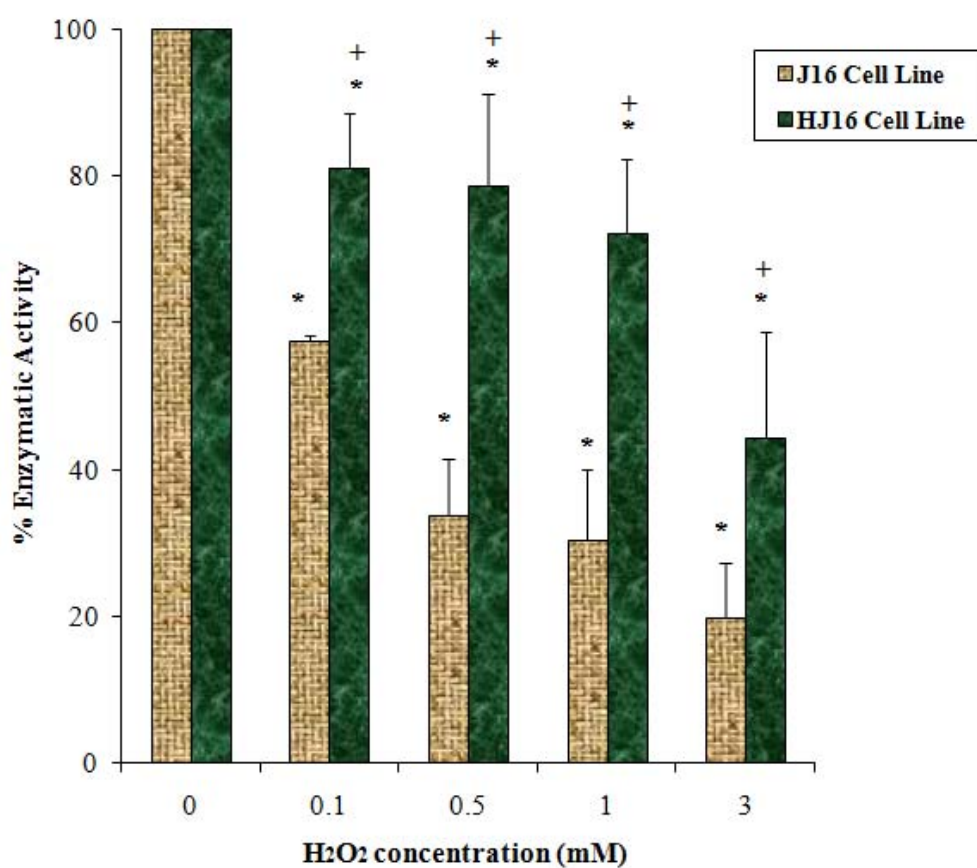


Figure 3.1 :

Effect of different concentrations of H₂O₂ treatment on the viable cells in J16 (parental) and HJ16 (H₂O₂-resistant) cell lines.

MTT analysis (see section 2.4) was performed 24 h following H₂O₂ treatment. These results are expressed as mean \pm standard deviation (n=3)

* : $p < 0.05$ significantly different when compared with corresponding control of the same cell line.

+ : significantly different when compared with J16 cell line of the same treatment.

3.1.2 Flow cytometric analysis

Since two mechanisms of cell death occur within the cells, flow cytometric analysis was performed to distinguish between the two mechanisms. Cells either die by necrosis (accidental form of cell death) or alternatively by apoptosis (programmed form of cell death). The dual staining of the cells with Annexin-V / Propidium iodide (PI) will allow to gate the cells to determine the percentage of live, apoptotic, and necrotic cells.

An example of such analysis is illustrated in figure 3.2. In this example J16 and HJ16 cell lines were either untreated or treated with H_2O_2 concentrations of 0.5 and 3 mM. As displayed in figure 3.2, there are 4 compartments. The lower left quadrant indicates the total of live cells (i.e. Annexin-V negative - PI negative), whereas the lower right quadrant indicates apoptosis (i.e. Annexin-V positive - PI negative). The upper right (i.e. Annexin-V positive - PI positive) and upper left (i.e. Annexin-V negative - PI positive) quadrants indicate primary and secondary necrosis, respectively.

Flow cytometric analysis (see figure 3.3) carried out following dual Annexin-V / PI staining of both J16 and HJ16 cell lines 24 h after H_2O_2 treatment confirms our previous results determined with MTT analysis. Overall, the flow cytometric analysis revealed that neither J16 nor HJ16 cell lines undergo H_2O_2 -mediated apoptotic cell death. Furthermore in both cell lines, H_2O_2 induced a concentration-dependent necrotic cell death. However the comparison of the percentage of necrotic cell death in both cell lines following H_2O_2 treatment clearly demonstrated that the HJ16 cell line has significantly higher resistance to the oxidising agent (i.e. up to 3 mM H_2O_2) than the J16 cell line. Indeed in the J16 cell line, the cytotoxicity of H_2O_2 was already apparent at a concentration as low as 0.5 mM, since the population of live cells was decreased from 90% to 50%. At a higher concentration of 3 mM H_2O_2 , almost no live J16 cells were present in the flow cytometric chart. The dose-dependent decrease in live J16 cells following H_2O_2 treatment also coincided with a reciprocal increase in the percentage of necrotic cells, strongly suggesting that necrosis is the primary mode of cell death induced by H_2O_2 in this cell line.

In summary, the flow cytometric analysis was in agreement with the MTT analysis, as both assays confirmed that the HJ16 cell line possessed higher resistance to H_2O_2 than the parental J16 cell line.

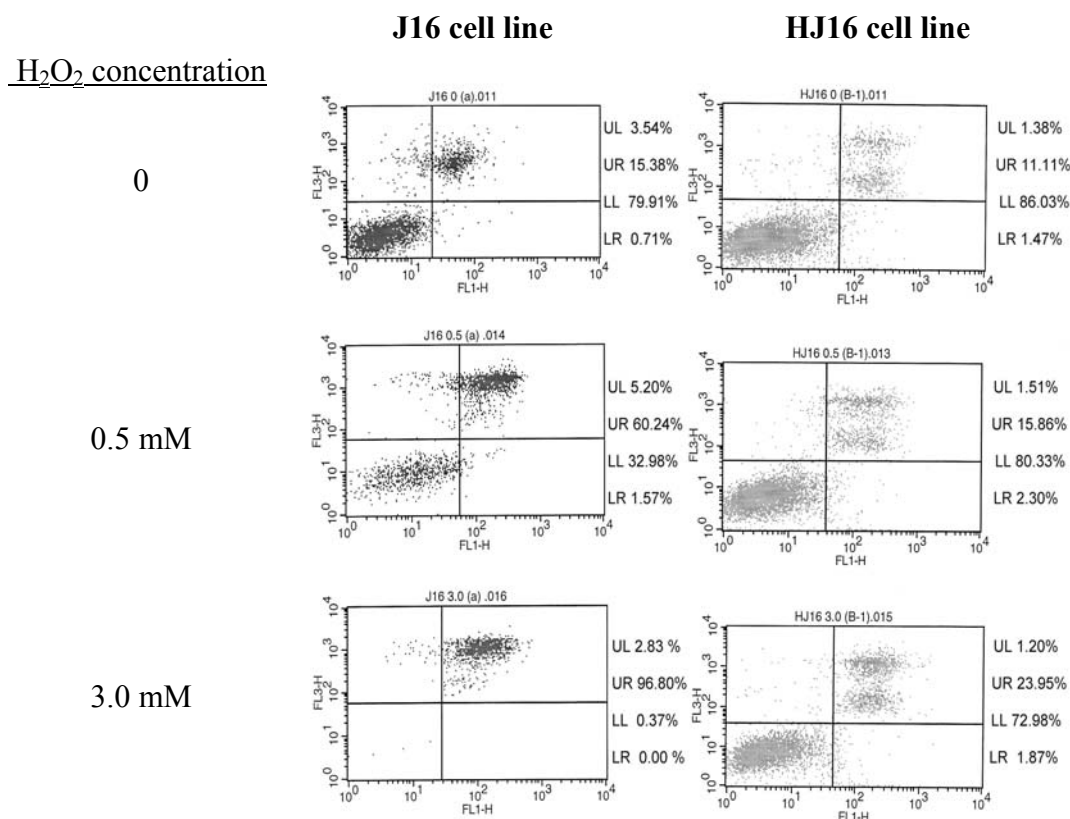


Figure 3.2 :

An example of the evaluation of flow cytometry analysis following H₂O₂ treatment (i.e. 0.5, and 3 mM) of J16 and HJ16 cell lines.

The analysis (see section 2.5) was performed 24 h after H₂O₂ treatment following dual Annexin-V/PI staining. Live cells are situated in the lower left quadrant (LL), whereas apoptotic cells are situated in the lower right quadrant (LR), and primary and secondary necrotic cells are situated in the upper right (UR) and upper left (UL) quadrant, respectively.

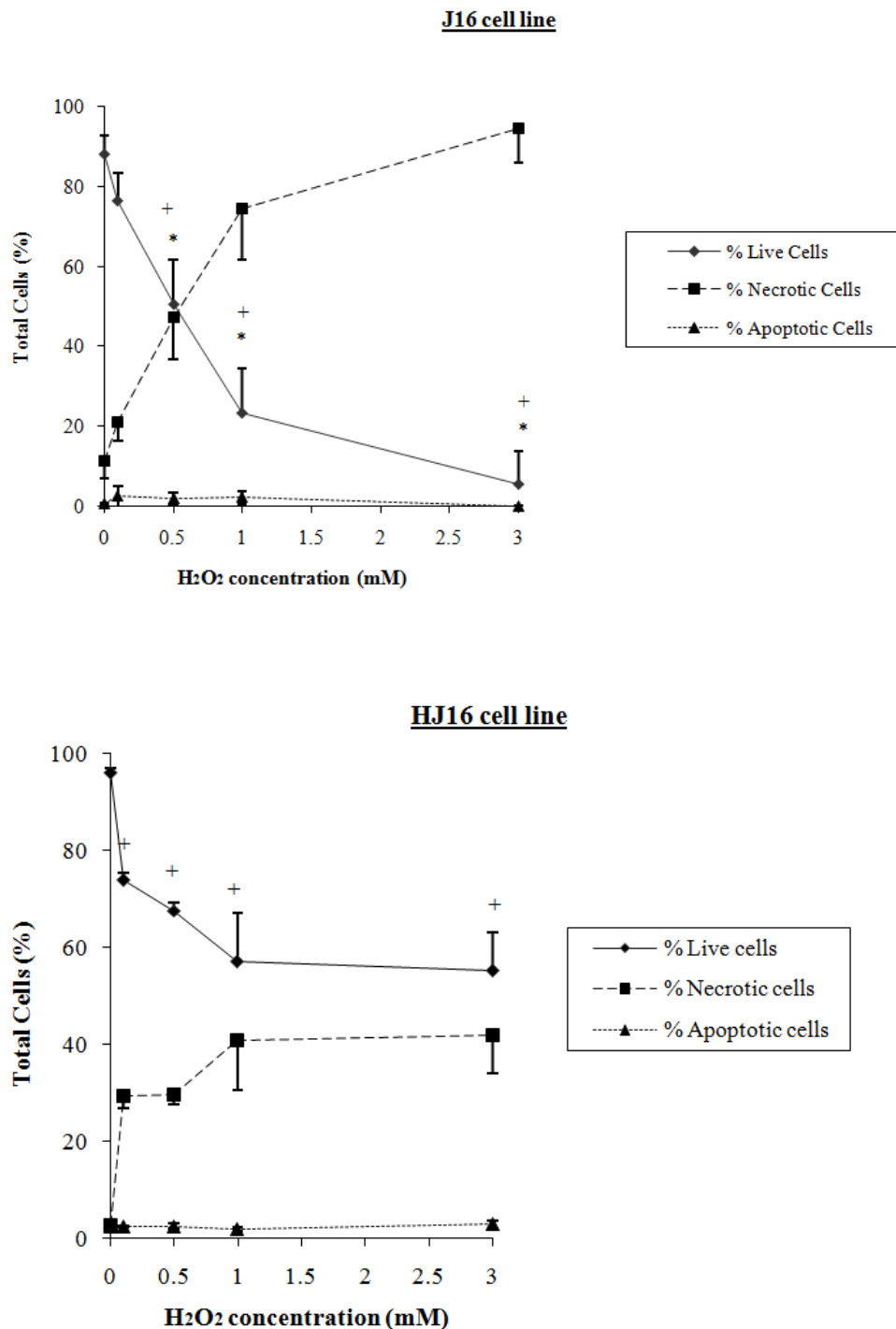


Figure 3.3 :

The effect of H₂O₂ on the percentage of live, necrosis, and apoptosis in J16 and HJ16 cell lines. Flow cytometric analysis (see section 2.5) was performed 24 h after H₂O₂ treatment following dual Annexin-V/PI staining. The results are expressed as mean \pm standard deviation (n=3)

+ : $p < 0.05$ significantly different between treated and corresponding controls.

* : $p < 0.05$ significantly different from HJ16 cell line (Live cells).

3.2 The role of total intracellular glutathione

The total intracellular glutathione (GSH/GSSG) system acts as a homeostatic redox buffer (see section 1.4.1.1) providing a major constitutive defence against oxidants (Applegate *et al*, 1992). Yiakouvaki (2003) showed that while the basal level activity of GPx enzyme in the HJ16 cell line is 2-fold higher than in J16 cell line, catalase activity is only 1.2-fold higher in HJ16 cells (non-significant). The higher GPx activity is likely to contribute to higher resistance of the HJ16 to H₂O₂-mediated toxicity. To determine whether the total intracellular levels of glutathione play a role in increased resistance of HJ16 cell line to H₂O₂, the basal GSH/GSSG level was monitored in both parental (J16) and H₂O₂ – resistant (HJ16) cell lines. Furthermore an attempt was made to deplete GSH/GSSG in both cell lines (i.e. by BSO, see next section) to demonstrate the possible link between GSH/GSSG and susceptibility of both cell lines to H₂O₂-mediated cytotoxicity.

3.2.1 The effect of Buthionine-[S,R]sulfoximine (BSO) treatment on J16 and HJ16 cells

Buthionine-[S,R]sulfoximine (BSO) is known to be a relatively non-toxic compound whose effect is apparently restricted to the inhibition of γ -glutamylcysteine synthetase. *In vivo* studies have shown that the administration of BSO to mice for several weeks has no undesirable effects other than glutathione depletion (Dethmers and Meister, 1981).

To evaluate the toxicity of BSO in our cell lines, MTT analysis (see section 2.4) was performed. J16 and HJ16 cell lines were treated for 18 h with a range of BSO (see section 2.3.2) concentrations (i.e. 2, 5, 15, 25, 50, and 250 μ M). The results (see figure 3.4) clearly showed that in both cell lines the compound has no toxicity towards the cells at concentrations up to 250 μ M.

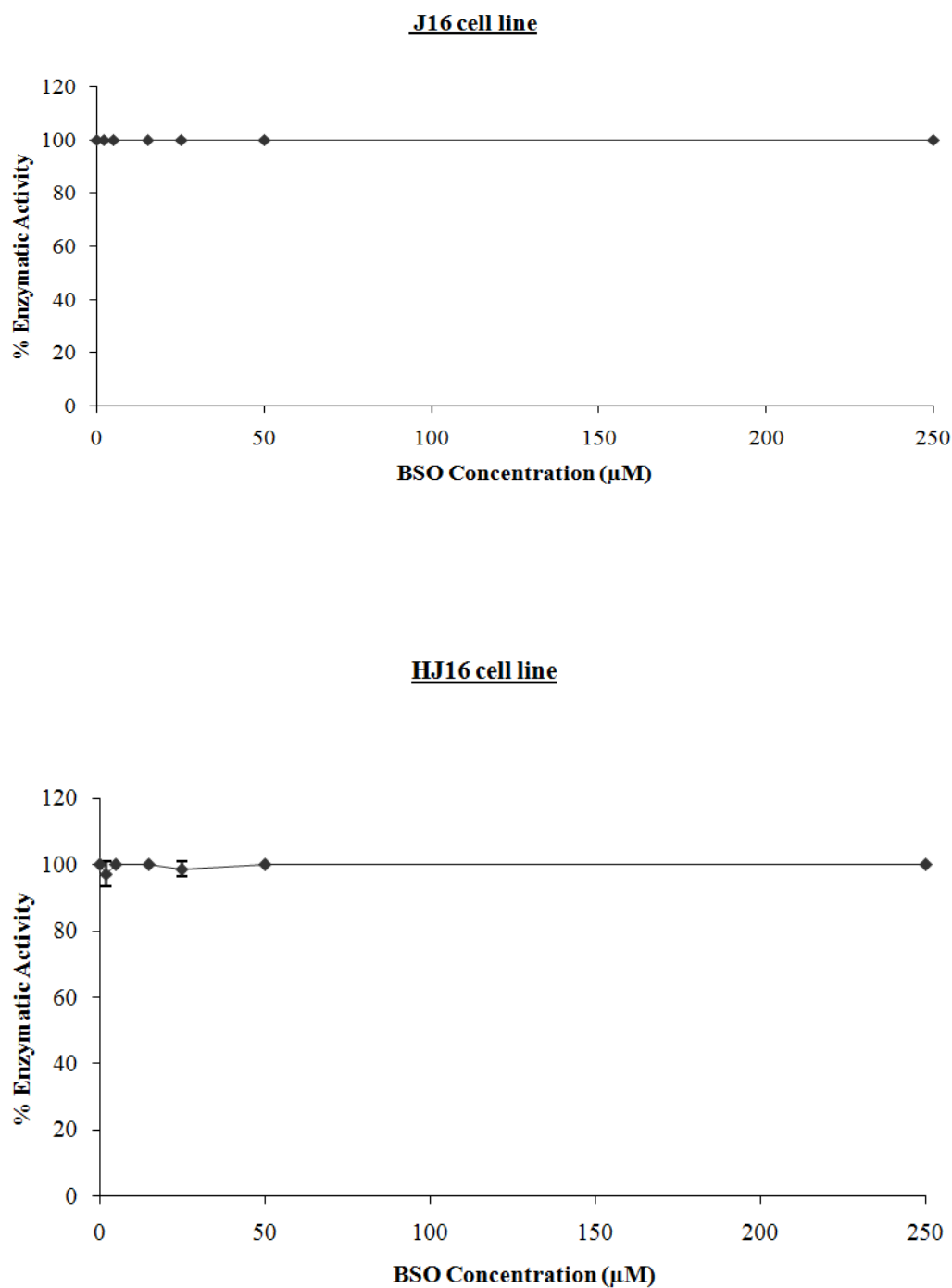


Figure 3.4 :

Effect of BSO on the viable cells in both J16 and HJ16 cell lines.

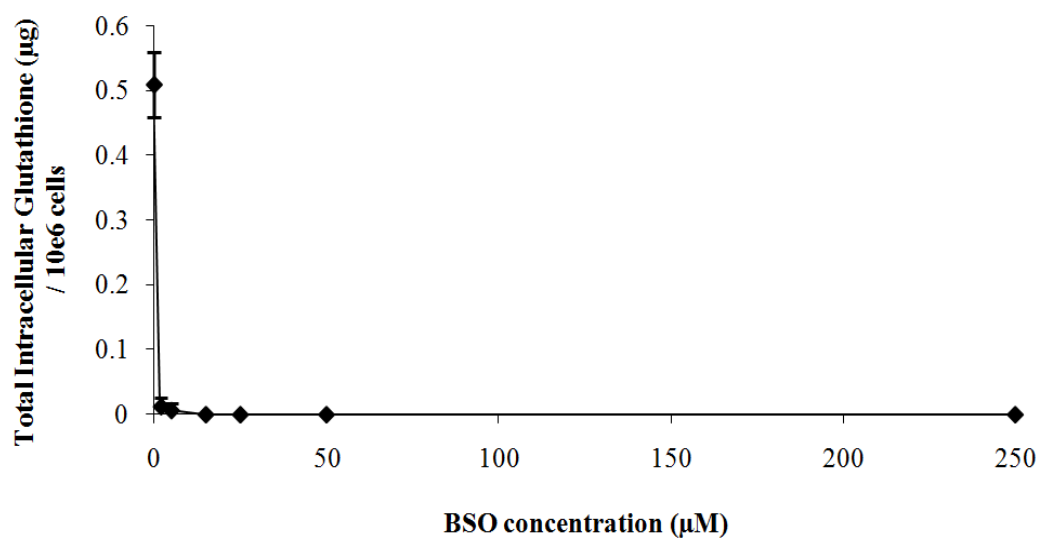
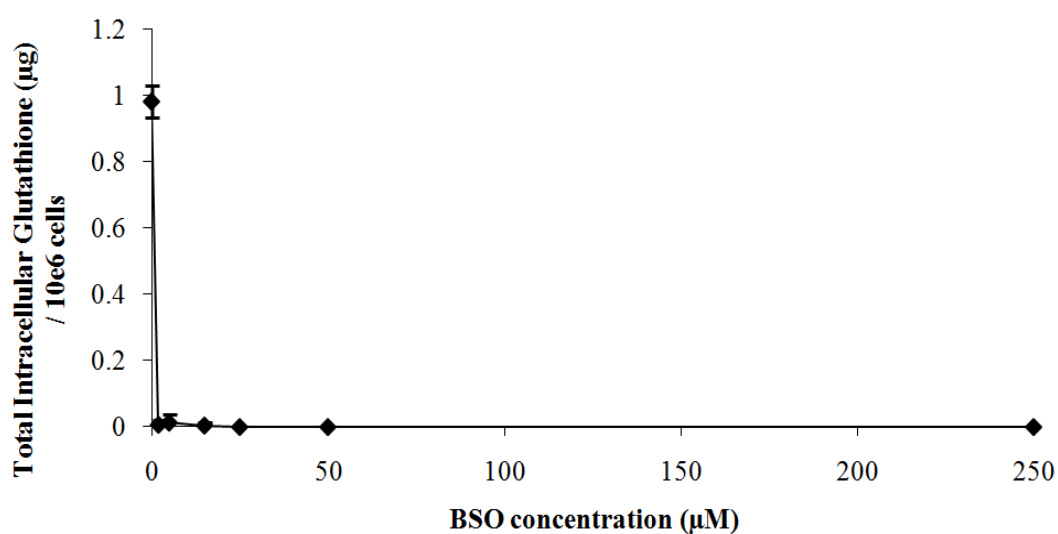
MTT analysis (see section 2.4) was performed 18 h following treatment of both cell lines with BSO at concentrations of 2, 5, 15, 25, 50, and 250 μM for 18 h. The results were expressed as mean \pm standard deviation (n=3).

3.2.2 The effect of BSO on the total intracellular levels of glutathione in J16 and HJ16 cells

To study the modulation of GSH/GSSG by increasing concentrations of BSO, the GSH/GSSG was determined using Tietze's method (see section 2.7). Furthermore it was important to check the differences in basal intracellular glutathione levels that might contribute to the higher resistance of HJ16 cell line to H₂O₂ when compared to J16 cell lines. For this purpose both cell lines were treated with a range of concentrations of BSO (i.e. 2, 5, 15, 25, 50, and 250 μ M) and then assayed by Tietze's method to evaluate the intracellular glutathione levels. The GSH/GSSG level was then normalised by two methods: cell count [per 10⁶ cells] and protein concentration [per total protein (mg)]. The normalisation with both methods (see figure 3.5 and figure 3.6) showed that a dose of 25 μ M of BSO was sufficient to deplete the GSH/GSSG level in both J16 and HJ16 cell lines.

3.2.3 Basal levels of the total intracellular glutathione in J16 and HJ16 cell lines

The basal level of the GSH/GSSG was assessed in both cell lines by using Tietze's method. The normalisation with cell count and with protein concentrations (see figure 3.5 and figure 3.6) revealed that HJ16 cells possess significantly higher levels of intracellular glutathione than J16 cells. Indeed, the measurement of the intracellular glutathione in the HJ16 cell line was found to be 3.4-fold higher than in the J16 cell line (see table 3.1). Since in an independent study from our laboratory (i.e. Yiakouvaki, 2003), it was found that these two cell lines had considerable difference in their cell volume (i.e. J16 cells: 0.47 ± 0.08 pl and HJ16: 1.6 ± 0.19 pl), it was therefore concluded that the normalisation with cell count is an inaccurate method for estimating the basal level of the GSH/GSSG in these cell lines, and that the data normalised with protein concentration should be used instead.

J16 cell line**HJ16 cell line****Figure 3.5 :**

The normalisation of intracellular glutathione in J16 and HJ16 cell lines to cell count.

Both cell lines were treated with BSO for 18 h at concentration of 2, 5, 15, 25, 50, and 250 µM prior to intracellular glutathione measurements (see section 2.7). The results were expressed as mean \pm standard deviation (n=3).

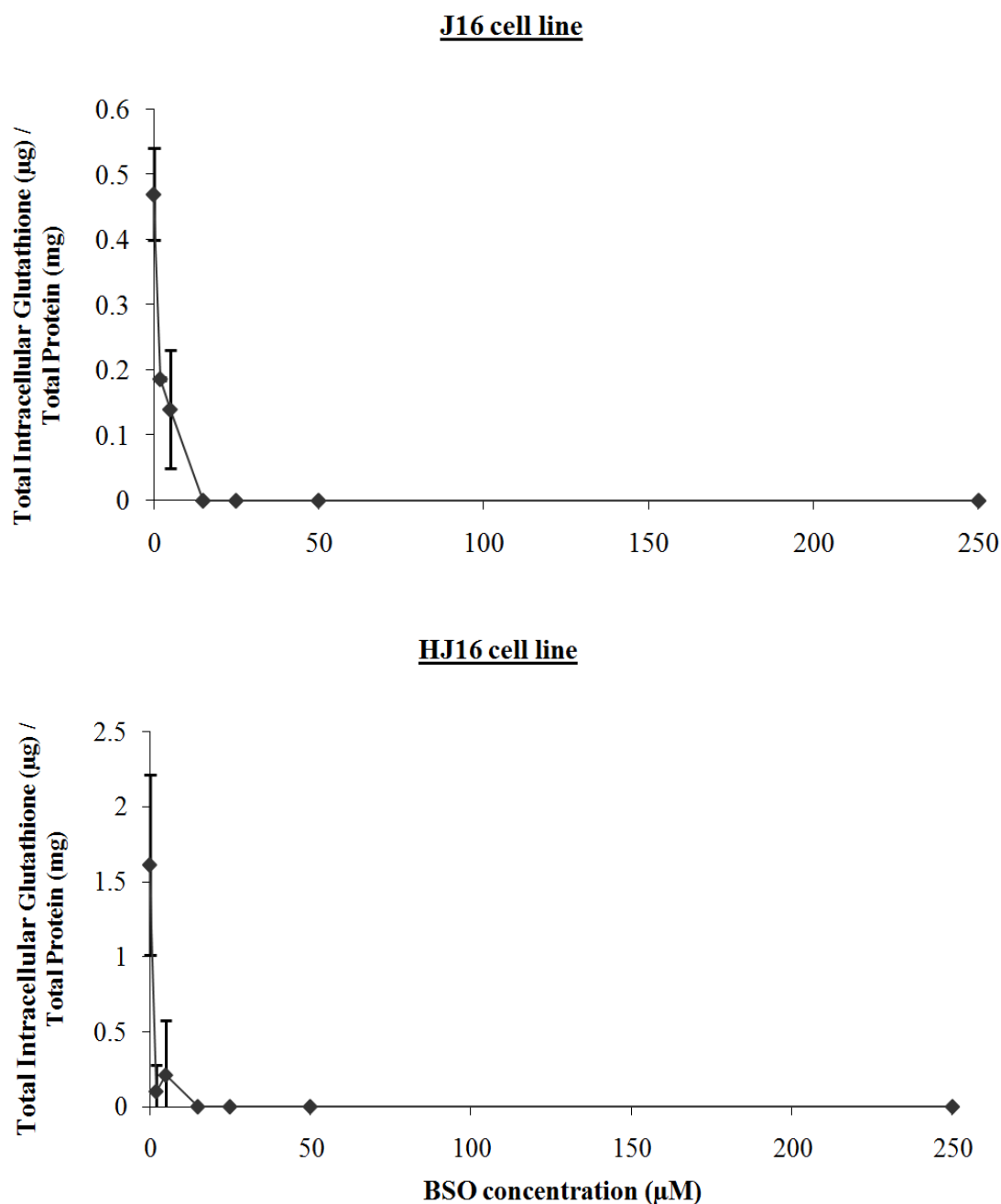


Figure 3.6 :

The normalisation of intracellular glutathione for J16 and HJ16 cell lines to total intracellular protein levels.

Both cell lines were treated with BSO for 18 h at concentration of 2, 5, 15, 25, 50, and 250 μM prior to intracellular glutathione measurements (see section 2.7). The results were expressed as mean ± standard deviation (n=3).

Table 3.1 :

Effect of BSO on the total intracellular glutathione content of J16 and HJ16 cell line.

Treatment	J16 Cell Line (μM glutathione / mg protein)	HJ16 Cell Line (μM glutathione / mg protein)
Control	0.47 ± 0.07	1.61 ± 0.67 *
25 μM BSO for 18 h	0	0

Cells were pre-treated with 25 μM BSO for 18 h as described in section 2.7. The total glutathione levels were assayed by Tietze's Method (see section 2.7) and normalised to total cellular protein. The results were expressed as mean \pm standard deviation (n=4).

* : $p < 0.05$ significantly different when compared with J16 cell line.

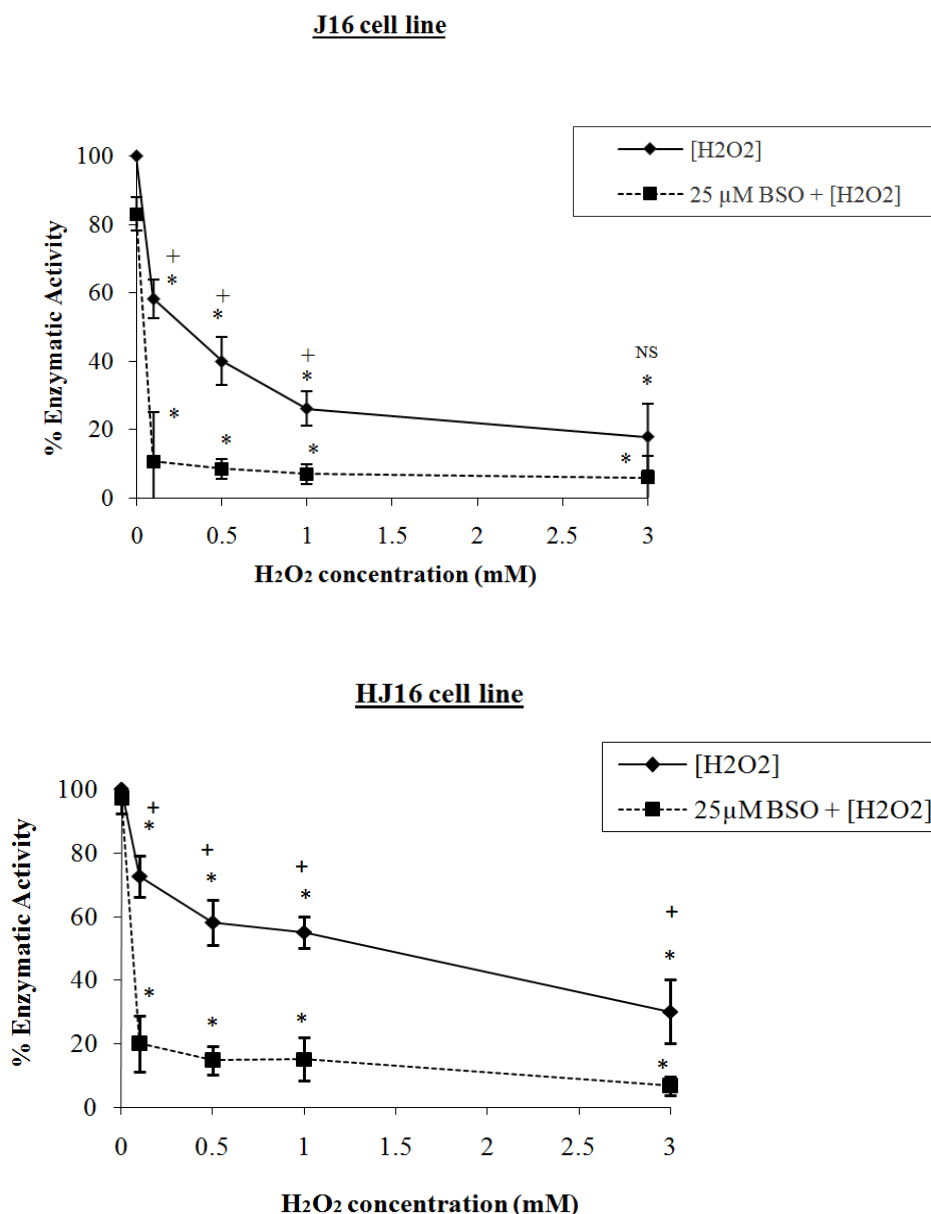
3.2.4 The susceptibility of both cell lines to H₂O₂ following glutathione depletion by BSO

To investigate the susceptibility of both cell lines to H₂O₂ treatment following the depletion of the GSH/GSSG, J16 and HJ16 cell lines were first incubated for 18 h with 25 μ M BSO and then treated with H₂O₂ at concentrations of 0.1, 0.5, 1.0, and 3 mM. The MTT analysis was then performed to determine the levels of cytotoxicity following these various treatments. The MTT results (see figure 3.7) showed that the susceptibility of the J16 cell line to a range of concentrations of H₂O₂ increases following the depletion of the GSH/GSSG by BSO. In HJ16 cells (see figure 3.7) the depletion of the GSH/GSSG also lead to enhanced cytotoxicity of the H₂O₂ treatment.

The MTT results were also confirmed by flow cytometric analysis using H₂O₂ doses up to 1 mM only, since the H₂O₂ dose of 3 mM was lethal to the J16 cell line. We have introduced to the treatments the H₂O₂ dose of 0.05 mM; therefore the concentrations of H₂O₂ used for flow cytometric analysis became 0.05, 0.1, 0.5, and 1.0 mM. The results obtained from flow cytometric analysis (see figure 3.8) confirmed the results shown by MTT analysis. Indeed in both cell lines, the susceptibility of cells to necrotic cell death increased after various doses of H₂O₂ following the depletion of the GSH/GSSG by 25 μ M BSO. The cytotoxicity was significantly different in both the J16 and the HJ16 cell lines at all concentrations of H₂O₂ used.

3.2.5 Levels of total intracellular glutathione in J16 and HJ16 cell lines after the treatment of H₂O₂

The levels of total intracellular glutathione were determined following H₂O₂ treatment in J16 and HJ16 cell lines following the observation that the susceptibility of both cell lines to a range of concentrations of H₂O₂ increases following the depletion of the GSH/GSSG by BSO (see section 3.2.2). Our results (see figure 3.9) showed that H₂O₂ doses of higher than 0.1 mM depletes significantly the amount of total intracellular glutathione in the J16 cell line. However in HJ16 cells, H₂O₂ treatment only decreased to half the GSH/GSSG.

**Figure 3.7 :**

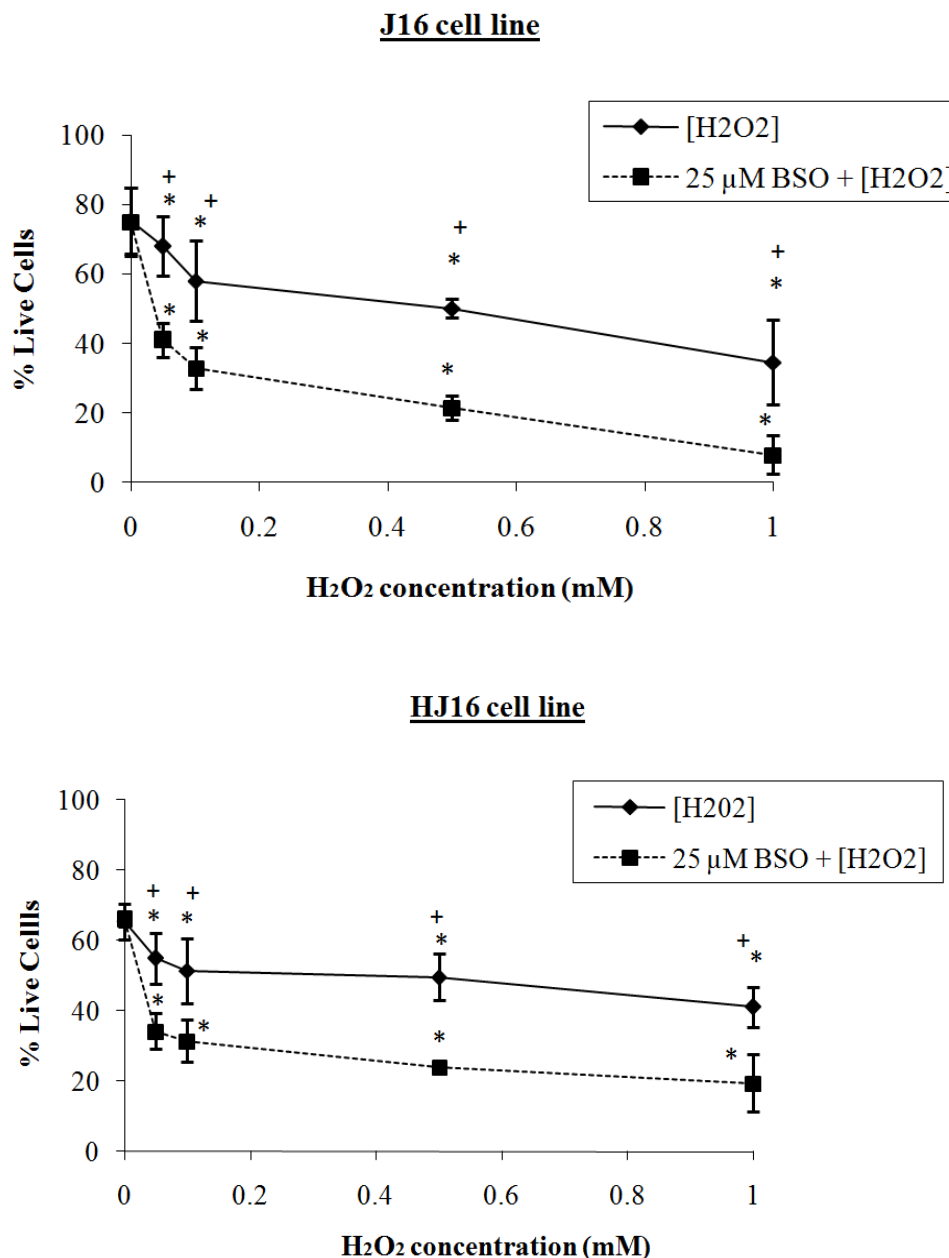
The evaluation of the susceptibility of J16 and HJ16 cell lines to H₂O₂ after the depletion of intracellular glutathione (Analysis : MTT).

Cells were treated overnight with BSO (25 μM) and then treated with various concentrations of H₂O₂ (0.1, 0.5, 1.0, and 3 mM). MTT analysis (see section 2.4) was performed 24 h following H₂O₂ treatment. The results are expressed as mean ± standard deviation (n=3).

* : $p < 0.05$ significantly different when compared with corresponding control of the same treatment.

+ : $p < 0.05$ significantly different when compared with cells treated with BSO prior to H₂O₂ treatment.

NS : non-significant different when compared with cells treated with BSO prior to H₂O₂ treatment

**Figure 3.8 :**

The determination of the susceptibility of J16 and HJ16 cell lines to H₂O₂ after the depletion of total intracellular glutathione (Flow cytometric analysis).

Cells were treated overnight with BSO (25 μM) and then treated with various concentrations of H₂O₂ (0.05, 0.1, 0.5, and 1.0 mM). Flow cytometry analysis (see section 2.5) was performed 24 h following H₂O₂ treatment. The results are expressed as mean ± standard deviation (n=3).

* : p < 0.05 significantly different when compared with corresponding control of the same treatment.

+ : p < 0.05 significantly different when compared with cells treated with BSO prior to H₂O₂ treatment.

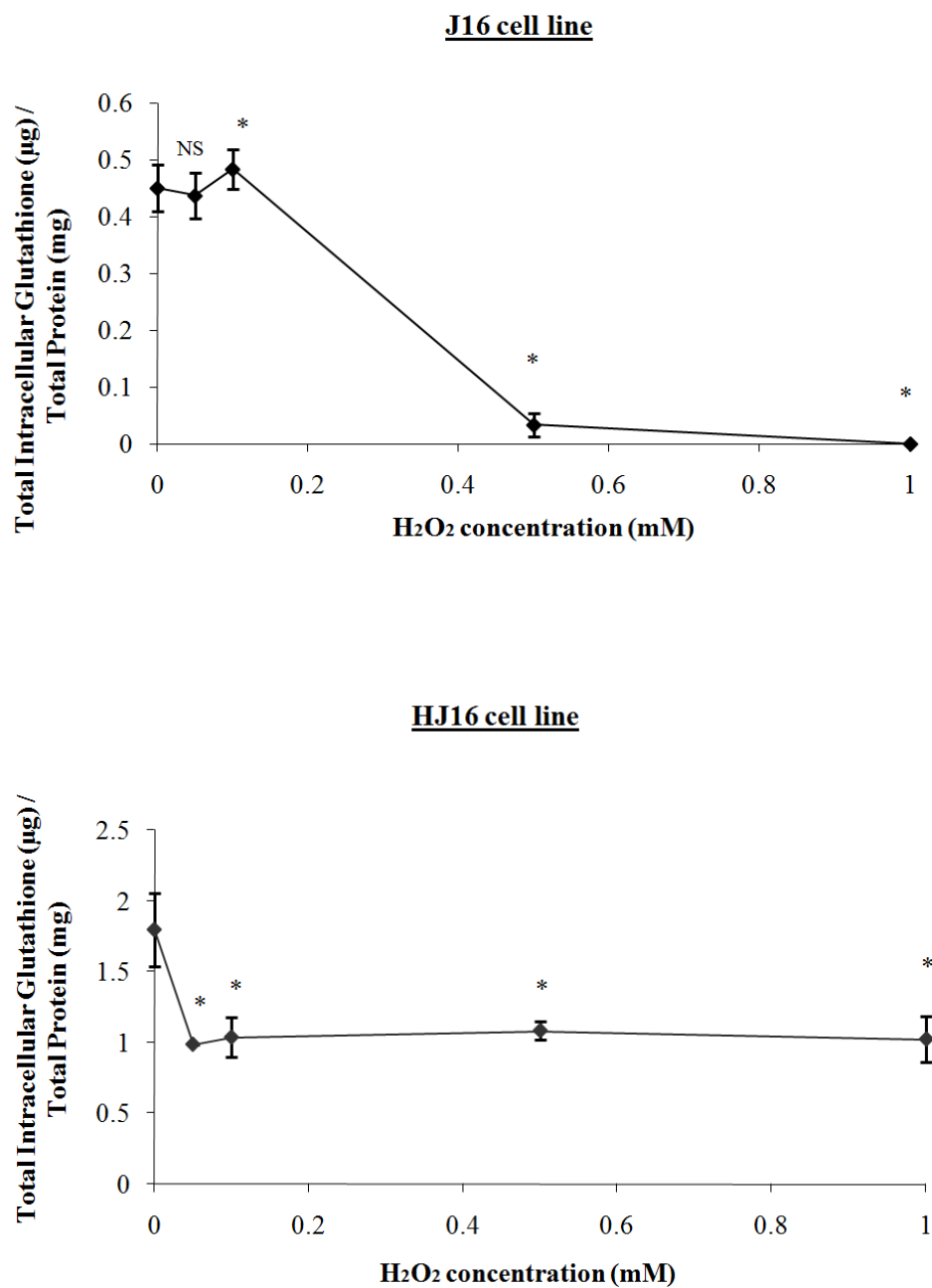


Figure 3.9 :

The determination of the levels of glutathione after the treatment with H₂O₂.

Cells were treated with H₂O₂ (0, 0.05, 0.1, 0.5, 1.0mM) as described in Materials and Methods and the total glutathione levels were assayed by Tietze's Method (see section 2.7) after the H₂O₂ treatment by 24 h. The results were expressed as mean \pm standard deviation (n=3).

* : p < 0.05 significantly different between treated and the corresponding control.

NS : non-significant difference from the corresponding control.

The results suggest that chronic exposure of HJ16 cells to H₂O₂ provokes an adaptive mechanism preventing the total depletion of total intracellular glutathione in these cells. This will almost certainly contribute to the resistance of HJ16 cells to doses as high as 1mM H₂O₂.

3.3 Characterisation of the response of NF- κ B to H₂O₂

As mentioned earlier (see section 1.6.5), the inducibility of the NF- κ B complex in response to H₂O₂ is cell-specific. Furthermore it is not clear whether this response will be lost if cells are chronically adapted to H₂O₂ treatment, in the case of the HJ16 cell line. Therefore the inducibility of NF- κ B complex, measured by Electrophoretic Mobility Shift Assay (EMSA) and immunocytochemistry was investigated in both J16 and HJ16 cell lines following H₂O₂ treatment.

3.3.1 The induction of NF- κ B complex in the J16 and HJ16 cell lines

After the performance of supershift analysis it was found that the first complex (CI) is the classical NF- κ B complex (RelA / p50), and the second complex (CII) appears to be p50 / p50 homodimer (A.Al-Qenaei MPhil Thesis, 2004 – University of Bath). This result was compatible with other studies that have been previously performed with other cell lines including Jurkat cells (Ginn-Pease and Whisler, 1996; Schoonbroodt *et al*, 2000; Gilston *et al*, 2001; Shin *et al*, 2004).

After 1 hour of various treatments of H₂O₂ (i.e. 0.5, and 1.0 mM), the induction of NF- κ B complex binding was observed in J16 cell line (see figure 3.10). The induction of NF- κ B in J16 cells appeared to be weak compared to HJ16 cell line. Nevertheless the NF- κ B complex binding by H₂O₂ was dose-dependent in J16 cells, as shown by the quantification of the bands (see table 3.2). The HJ16 cell line was treated with the same concentrations of H₂O₂ (0.5, and 1.0 mM). The basal NF- κ B complex binding was strongly induced in both concentration used (see figure 3.10 and table 3.2). These results confirm that NF- κ B complex is present and induced by H₂O₂ in both J16 and HJ16 cells, although the induction was higher in HJ16 cells.

3.3.2 Characterisation of the response of NF- κ B and Oct-1 to H₂O₂ treatment by immunocytochemistry

To confirm the previous results with EMSA, both J16 and HJ16 cells were treated with an intermediate dose, i.e. 0.5 mM H₂O₂, and subsequently the cells were incubated with 1, 6, and 24 h in condition medium and then immunocytochemistry of RelA (p65) and Oct-1 was performed (see section 2.10). The results shown in figure 3.11 and 3.12 reveal that p65 was situated in the cytoplasm, as expected.

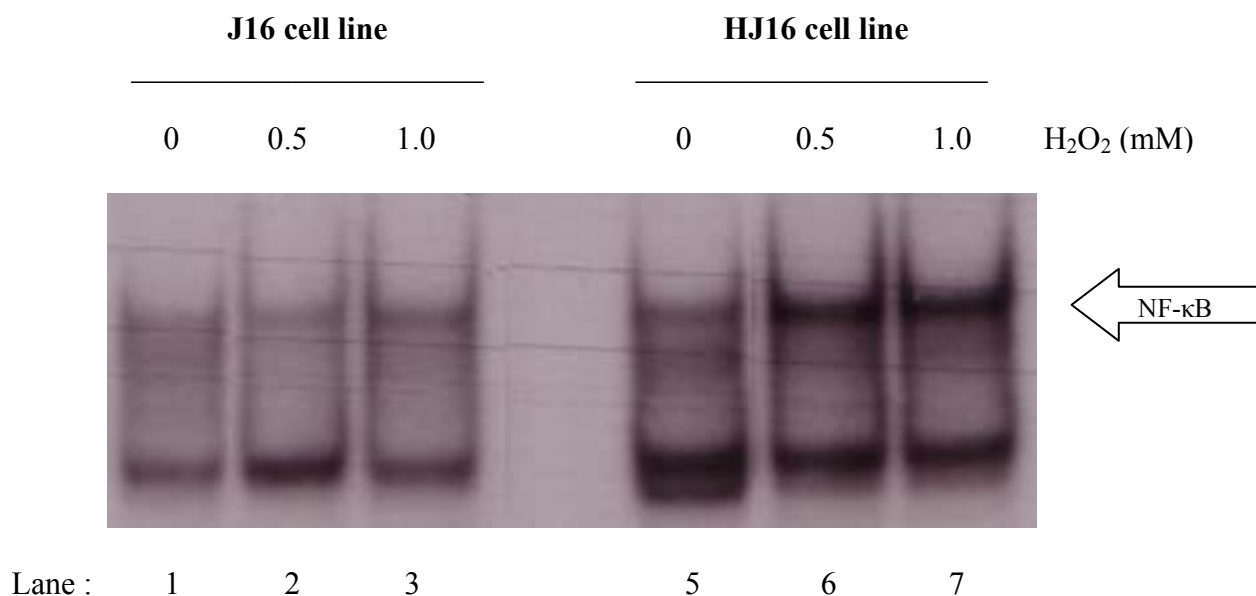


Figure 3.10 :

The induction of NF-κB activation in J16 and HJ16 cell lines 1 hour after H₂O₂ treatment.

[Analysed by electrophoretic mobility shift assay (EMSA) (see section 2.8)]

Lane 1 is the untreated J16 cell line (control), lanes 2 and 3 indicate the treatment of H₂O₂ (0.5 and 1.0 mM) respectively. Lane 5 is the untreated HJ16 cell line (control), lanes 6 and 7 indicate the treatment of H₂O₂ (0.5 and 1.0 mM) respectively.

The arrow indicates the position of the classical NF-κB complex (RelA / p50).

Table 3.2:

Numerical values of the quantification of the bands observed in Figure 3.11 (HJ16 and J16 cell line).

H₂O₂ Concentration (mM)	J16 cell line	HJ16 cell line
0	100 %	100 %
0.5	109 %	143 %
1.0	128 %	158 %

The bands were scanned and the quantification was assessed (see section 2.12.4) using LabImage software - Version 2.7.2 (Kapelan Bio-Imaging Solutions, Germany).

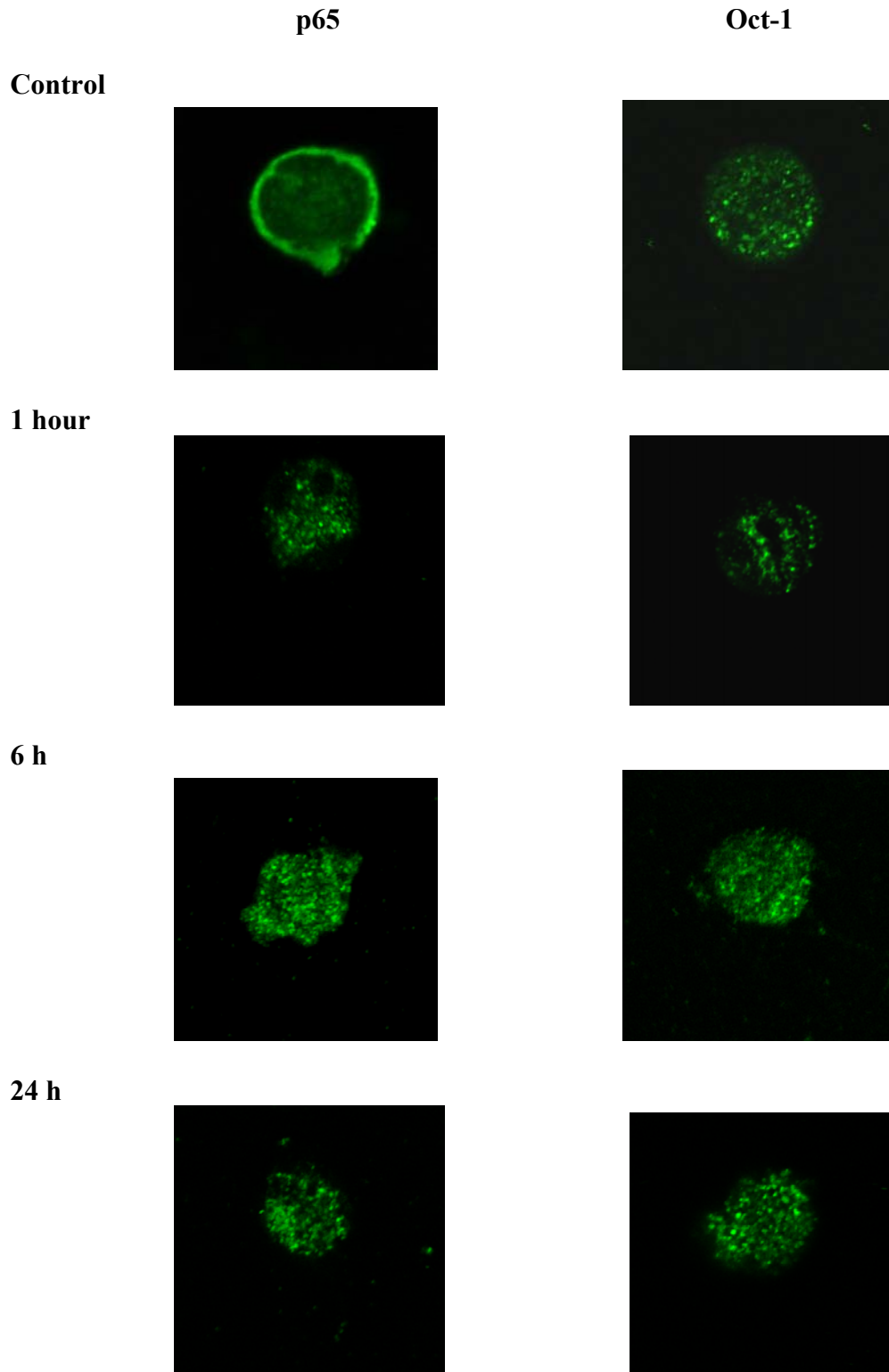


Figure 3.11 :
Localisation of RelA (p65) and Oct-1 following H₂O₂ treatment in J16 cell line.

J16 cells were treated with 0.5 mM of H₂O₂ and processed for immunochemistry (see section 2.13) at 1, 6, and 24 h post-treatment as described in section 2.13. The photographs are representative of three experiments.

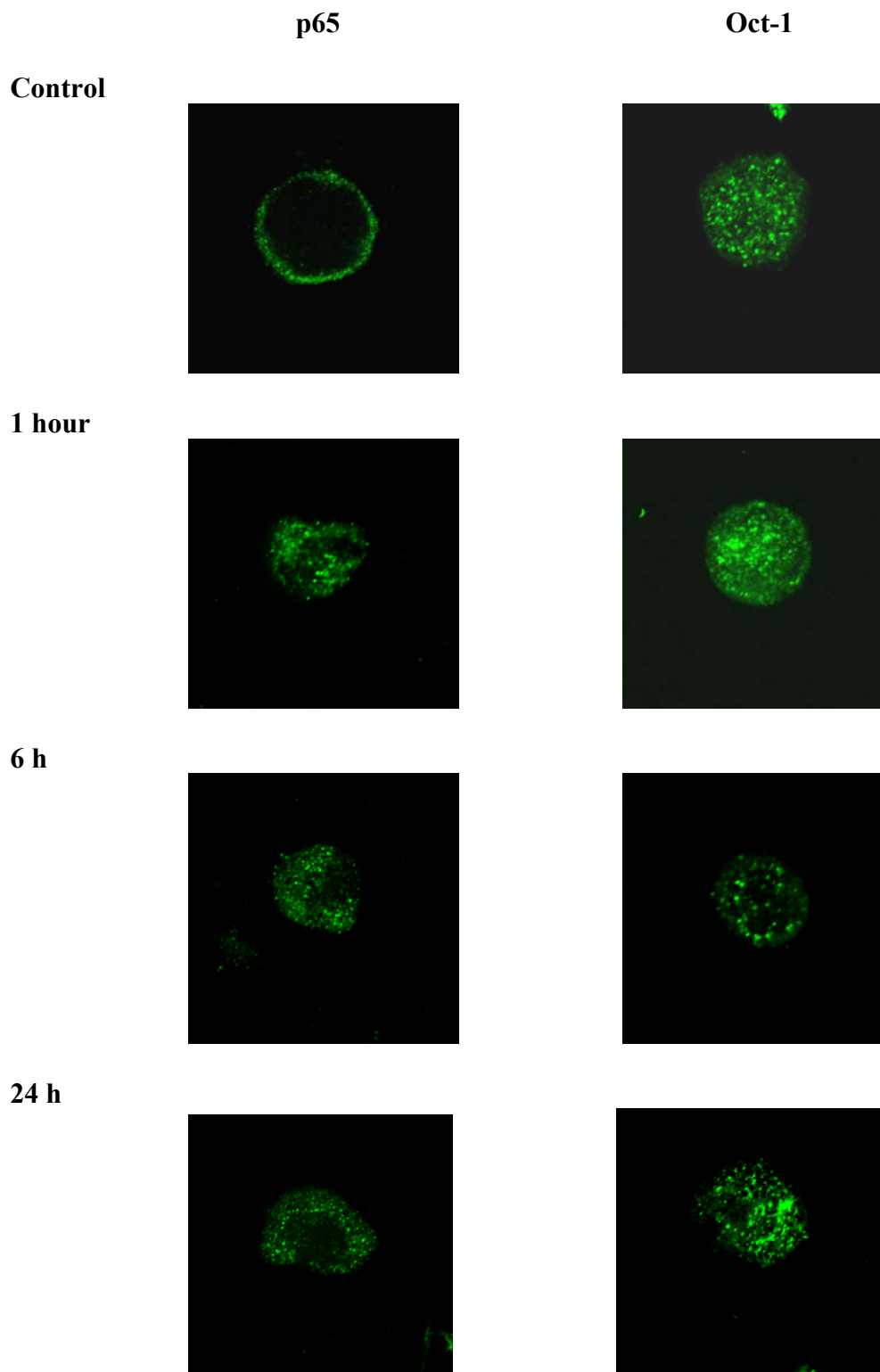


Figure 3.12 :

Localisation of RelA (p65) and Oct-1 following H_2O_2 treatment in HJ16 cell line.

HJ16 cells were treated with 0.5 mM of H_2O_2 and processed for immunochemistry (see section 2.13) at 1, 6, and 24 h post-treatment as described in section 2.13. The photographs are representative of three experiments.

Following H₂O₂ treatment, p65 translocated to the nucleus as early as 1 hour post-treatment and remained in the nucleus for at least 24 h after treatment. Studies with NF- κ B and UVA in our laboratory have shown that UVA damages the nuclear membrane leading to the leakage of freshly translocated NF- κ B to the cytosol. This was monitored by parallel leakage of nuclear Oct-1 to the cytosol (Reelfs *et al*, 2004). We therefore used Oct-1 in this study, to monitor possible damage to the nuclear membranes by H₂O₂. Our results demonstrated that Oct-1, the ubiquitous nuclear protein in mammalian cells, remained nuclear before and after H₂O₂ treatment in both cell lines in agreement with the notion that H₂O₂ does not damage the nuclear membrane. Taken together, the results showed that H₂O₂ activates the NF- κ B translocation in both cell lines and confirmed the activation observed in EMSA.

3.4 The role of labile iron

Iron is a known catalyst of biological oxidation. Studies from this laboratory and others have demonstrated that both ‘basal’ and ‘oxidant-induced’ level of labile iron pool (LIP) could influence the susceptibility of cells to oxidative damage and cell death (e.g. Bissett *et al*, 1991; Zhong *et al*, 2004; Morliere *et al*, 1997).

For example in the case of acute exposure of skin to UVA, Zhong *et al*, (2004) from this laboratory, demonstrated that epidermal keratinocytes have higher resistance to UVA-induced oxidative damage and cell death than dermal fibroblasts presumably because both the ‘basal’ and ‘UVA-induced’ level of labile iron is dramatically lower in keratinocytes than fibroblasts. Furthermore the modulation of ‘basal’ and ‘UVA-induced’ level of LIP by either DFO (iron chelating) and/or hemin (iron loading) treatment significantly affected the extent of UVA-induced necrotic cell death in both cell lines and it was concluded that cellular susceptibility to UVA-induced necrotic cell death reflects the intracellular level of LIP.

The study carried out by Yiakouvaki (2003) using a Jurkat T cell model and H₂O₂, indicated that although cellular resistance to H₂O₂ is tightly associated with intracellular level of LIP, it is the ‘H₂O₂-induced’ rather than ‘basal’ level of LIP that is responsible for the increased susceptibility of cells to oxidative stress, although the underlying mechanism remained unclear. We therefore decided to further investigate this phenomenon in our cell lines.

3.4.1 The role of LIP in differential sensitivity of the J16 and HJ16 cells to H₂O₂ treatment

Figures 3.13 to 3.15 summarize the main finding of A. Yiakouvaki (PhD Thesis, 2003) that was repeated and confirmed and then complemented in the present study. The results demonstrated that the ‘basal’ level of LIP in both J16 and HJ16 cells are quite similar i.e. $3.08 \mu\text{M} \pm 0.59$ and $3.34 \mu\text{M} \pm 0.87$ respectively, but following H₂O₂ treatment (e.g. at a final concentration 0.5 mM), the ‘H₂O₂-induced’ level of LIP increases in both cell lines but to a lesser extent in HJ16 cells. The lower induction of H₂O₂-mediated LIP release in HJ16 cell line correlated with lower necrotic cell death (see table 3.3).

Table 3.3 :

The effect of H₂O₂-induced LIP on necrotic cell death in J16 and HJ16 cells.

Condition / Cell line	J16 cells	HJ16 cells
Basal LIP	3.08 $\mu\text{M} \pm 0.59$	3.34 $\mu\text{M} \pm 0.87$
H₂O₂-induced LIP	9.86 $\mu\text{M} \pm 0.15$ *	5.27 $\mu\text{M} \pm 1.12$ * ⁺
Fold increase in H₂O₂-induced LIP	3.2-fold increase	1.6-fold increase
Percentage necrotic cell death post-H₂O₂	47 % ± 11	30 % ± 2 ⁺

Note : Measurements of LIP were performed by CA-assay immediately after 0.5 mM of H₂O₂ treatment. The results are expressed as mean \pm standard deviation (n=3-8). Flow cytometric analysis (see section 2.5) was performed 24 h after H₂O₂ treatment following dual Annexin-V/PI staining. The results are expressed as mean \pm standard deviation (n=3)

* : p < 0.05 significantly different between treated and the corresponding control

+ : p < 0.05 significantly different from the corresponding J16 cell line.

To ascertain the importance of H₂O₂-induced labile iron release in modulating the susceptibility of cells to H₂O₂-induced necrotic cell death, both J16 and HJ16 were treated with DFO, a strong iron chelator or hemin (i.e. ferric haem) as a source of iron for 18 h prior to H₂O₂ treatment and then the level of LIP was measured following H₂O₂ treatment using the CA assay. The results demonstrated that DFO treatment abolishes both the ‘basal’ and ‘H₂O₂-induced’ LIP levels and necrotic cell death (see table 3.4a-b, figures 3.13 and 3.14) in both cell lines, consistent with the notion that iron chelation by DFO protects the cells against H₂O₂-induced necrotic cell death. In the case of hemin treatment, hemin alone (i.e. when not followed by H₂O₂ treatment) does not modulate the level of LIP in J16 cells but upon H₂O₂ treatment it causes a low increase in LIP that correlates with low necrosis (see table 3.4-a, figures 3.13 and 3.15). This is in agreement with previous studies by Balla and co-workers showing that the endothelium’s susceptibility to H₂O₂-mediated insults decreases following exposure to hemin or haemoglobin (Balla *et al*, 1992 and 1993). On the other hand, hemin treatment modulated both the basal and H₂O₂-induced LIP levels in HJ16 cells. The accumulation of high levels of LIP in HJ16 cells following hemin treatment increased their susceptibility to H₂O₂-induced damage since the level of necrosis significantly increased upon hemin- H₂O₂ treatment (see table 3.4b, figures 3.13 and 3.15).

Further investigation with time course analysis revealed that in J16 cells, hemin treatment (20 µM) transiently increases the LIP levels within the first 4 h up to 2.2-fold, after which it returns to normal levels (see table 3.5a). In the HJ16 cells, hemin treatment provokes higher accumulation of LIP that is sustained at least for 18 h. The hemin-mediated increase in LIP appeared also to be concentration-dependent in the HJ16 cells (see figure 3.16). Since the high accumulation of LIP in HJ16 cells following hemin treatment increases the percentage of necrotic cell death, it was concluded that the intracellular level of LIP may play a key role in determining the level of sensitivity of these cells to H₂O₂-mediated necrotic cell death.

To further demonstrate the strict-dependence of H₂O₂-induced necrotic cell death to LIP level present in the cells, hemin treatment (20 µM) for 18 h was followed by an additional treatment with 1 mM DFO for 2h. The latter treatment was expected to lower the hemin-mediated increase in LIP, leading to decreased necrosis by H₂O₂.

Table 3.4 a: LIP measurements and the % of necrosis in J16 cell line.

Condition (J16 cell line)	LIP (μM)	Percentage necrotic cell death
Control (Basal)	$3.08 \mu\text{M} \pm 0.59$	$11 \% \pm 5$
H_2O_2 -0.5mM	$9.86 \mu\text{M} \pm 0.15^*$	$47 \% \pm 11^*$
DFO-100 μM – 18 h	0^*	$0.53 \% \pm 0.12^*$
DFO-100 μM + H_2O_2 -0.5mM	0^*	$0.53 \% \pm 0.11^*$
Hemin-20 μM – 18 h	$2.93 \mu\text{M} \pm 0.73^{\text{NS}}$	$1.4 \% \pm 0.47^*$
Hemin-20 μM + H_2O_2 -0.5mM	$4.02 \mu\text{M} \pm 0.95^{\text{NS}}$	$27.2 \% \pm 0.8^*$

Table 3.4 b: LIP measurements and the % of necrosis in HJ16 cell line.

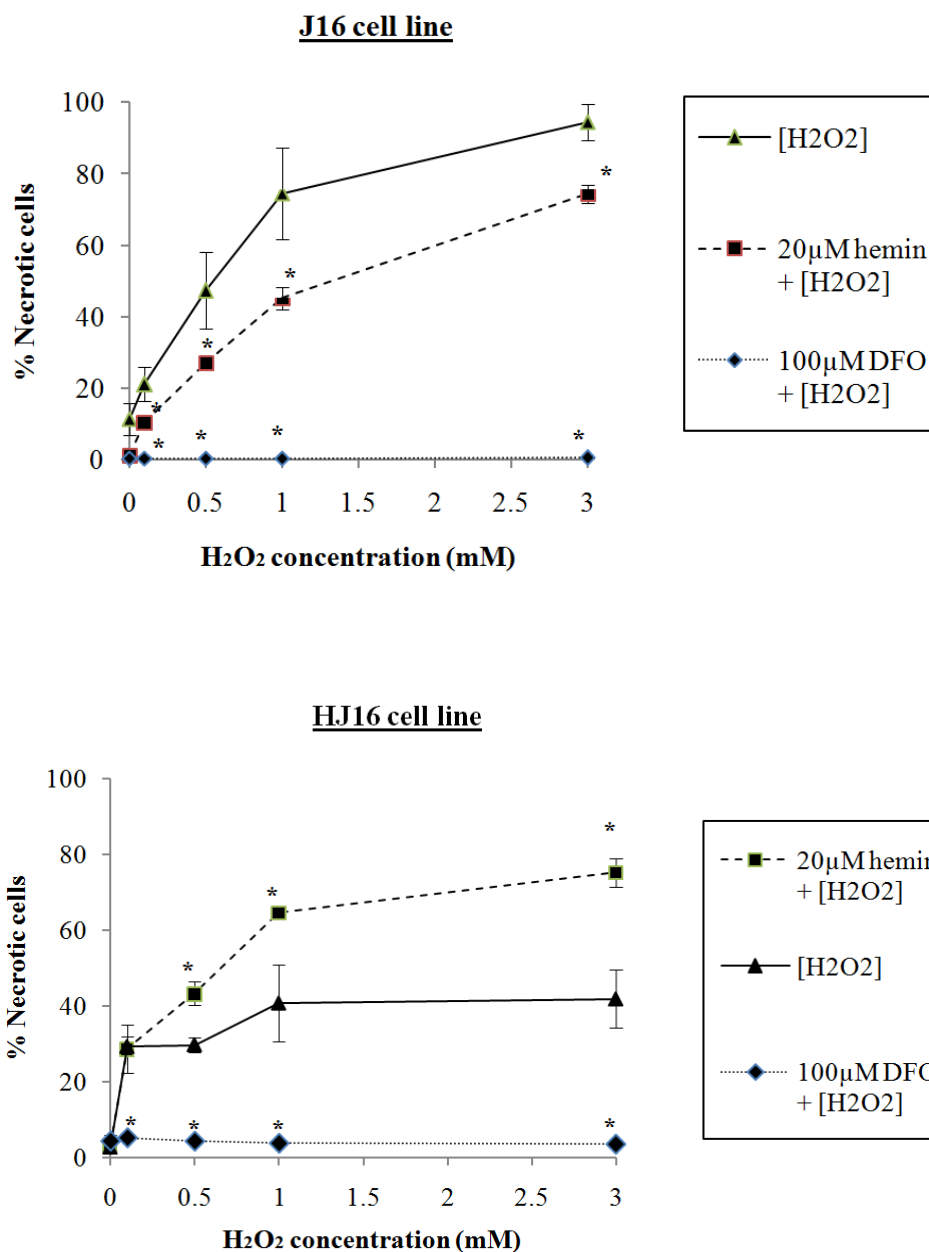
Condition (HJ16 cell line)	LIP (μM)	Percentage necrotic cell death
Control (Basal)	$3.34 \mu\text{M} \pm 0.87$	$3 \% \pm 0.6$
H_2O_2 -0.5mM	$5.27 \mu\text{M} \pm 1.12^{*+}$	$30 \% \pm 1.9^{*+}$
DFO-100 μM -18 h	0^*	$4.3 \% \pm 1.6^{\text{NS}}$
DFO-100 μM + H_2O_2 -0.5mM	0^*	$4.2 \% \pm 0.95^{\text{NS}}$
Hemin-20 μM – 18 h	$7.2 \mu\text{M} \pm 0.56^{*+}$	$3 \% \pm 0.76^{\text{NS}+}$
Hemin-20 μM + H_2O_2 -0.5mM	$12.2 \mu\text{M} \pm 0.34^{*+}$	$43.2 \% \pm 3.1^{*+}$

Note: Measurements of LIP were performed by CA-assay immediately after the specified treatments (above). The results are expressed as mean \pm standard deviation (n=3-8). Flow cytometric analysis (see section 2.5) was performed 24 h after H_2O_2 treatment following dual Annexin-V/PI staining. The results are expressed as mean \pm standard deviation (n=3).

* : $p < 0.05$ significantly different between treated and the corresponding control

NS : non-significantly different from the corresponding control.

+ : $p < 0.05$ significantly different from the corresponding J16 cell line.

**Figure 3.13 :**

The evaluation of the susceptibility of J16 and HJ16 cell lines to iron chelation and loading prior to H₂O₂ treatment (Flow cytometric analysis).

Cells were pretreated with either 100 µM DFO or 20 µM hemin for 18 h before H₂O₂ treatment. Flow cytometric analysis (see section 2.5) was performed 24 h after H₂O₂ treatment following dual Annexin-V/PI staining. These results are expressed as mean ± standard deviation (n=3).

* : p < 0.05 significantly different from the cells treated with H₂O₂ treatment alone.

NS : non-significant different from the cells treated with H₂O₂ treatment alone.

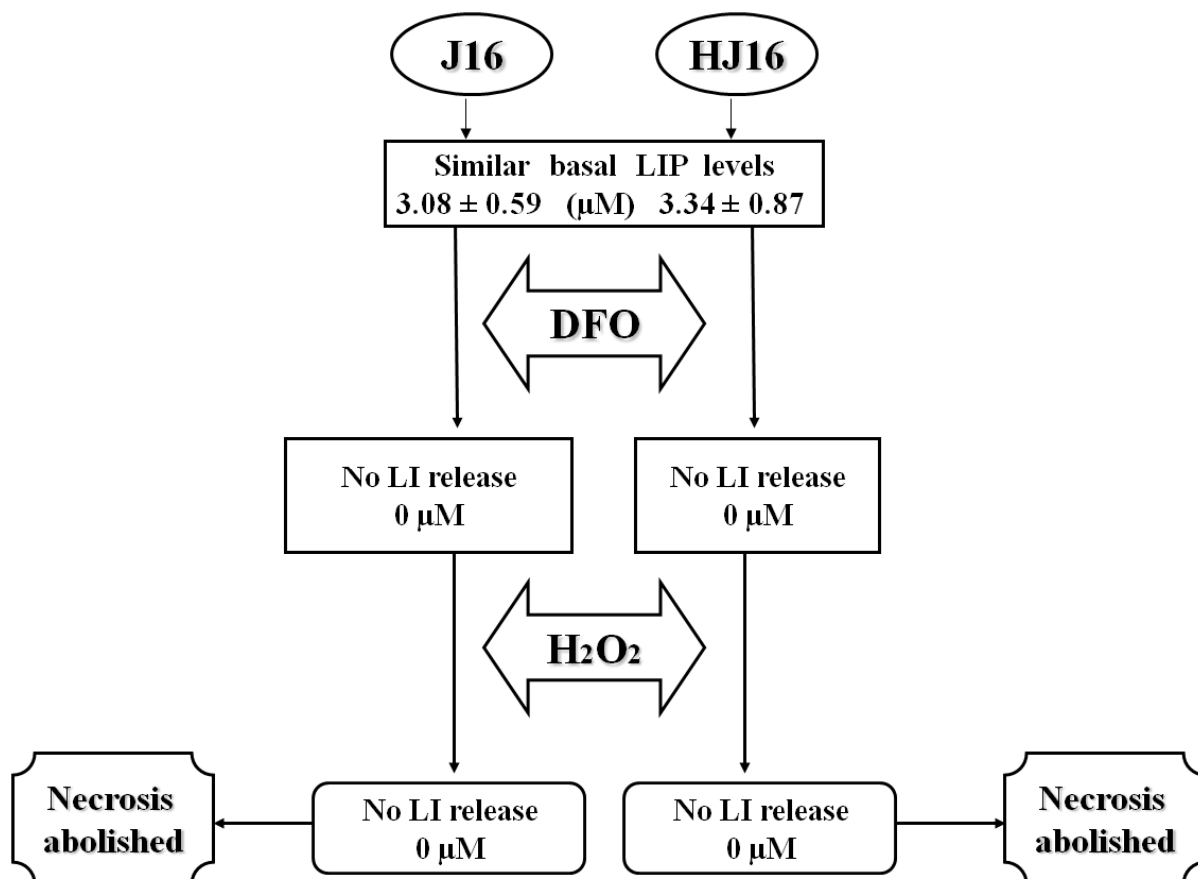


Figure 3.14:

Schematic representation of the effect of $\text{DFO} \pm \text{H}_2\text{O}_2$ treatment on labile iron pool (LIP) and the viability of J16 and HJ16 cells.

Both cell lines were either treated overnight with $100 \mu\text{M}$ DFO alone or $100 \mu\text{M}$ DFO for 18 h prior an intermediate dose of H_2O_2 (i.e. 0.5mM). The levels of LIP was determined (Yiakovaki, 2003) by a modification of the method developed by Epsztejn *et al* (1997). The level of necrosis was determined by flow cytometric analysis (see section 2.5).

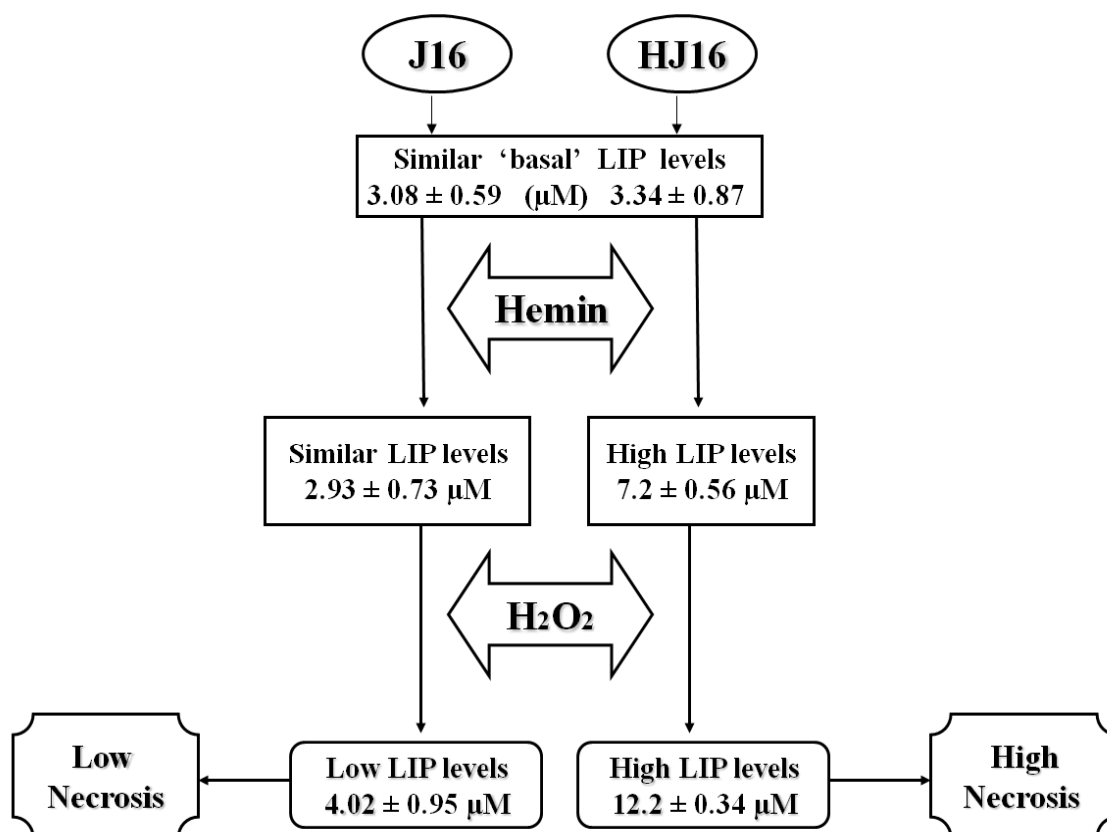


Figure 3.15:

Schematic representation of the effect of hemin \pm H₂O₂ treatment on labile iron pool (LIP) and the viability of J16 and HJ16 cells.

Both cell lines were either treated overnight with 20 μM hemin alone or 20 μM hemin for 18 h prior an intermediate dose of H₂O₂ (i.e. 0.5mM). The levels of LIP was determined by a modification of the method developed by Epsztejn *et al* (1997). The level of necrosis was determined by flow cytometric analysis (see section 2.5).

Table 3.5a: Time course of LIP measurements and the fold increase of LIP after 20 μ M hemin treatment of J16 cells.

Condition	LIP (μ M)	Fold increase
Basal - 0 h	3.3 μ M \pm 0.87	1
2 h	6.8 μ M \pm 1.6 *	2-fold increase
4 h	7.4 μ M \pm 1.8 *	2.2-fold increase
6 h	3.1 μ M \pm 0.53	Non-significant
8 h	3.5 μ M \pm 0.38	Non-significant
18 h	2.6 μ M \pm 0.42	Non-significant

Table 3.5b: Time course of LIP measurements and the fold increase of LIP after 20 μ M hemin treatment of HJ16 cells.

Condition	LIP (μ M)	Fold increase
Basal - 0 h	3.34 μ M \pm 0.87	1
2 h	11.8 μ M \pm 1.8 * ⁺	3.5-fold increase
4 h	11.2 μ M \pm 1.7 * ⁺	3.4-fold increase
6 h	14.1 μ M \pm 0.93 * ⁺	4.2-fold increase
8 h	10.3 μ M \pm 0.41 * ⁺	3.1-fold increase
18 h	7.2 μ M \pm 0.56 * ⁺	2.2-fold increase

Note : The LIP was monitored by Calcein assay following the treatment of J16 and HJ16 cells with 20 μ M hemin for various times (i.e. 2, 4, 6, 8 and 18 h). The results are expressed as mean \pm standard deviation (n=6-8).

* : p < 0.05 significantly different between treated and the corresponding control
 + : p < 0.05 significantly different from the corresponding J16 cell line.

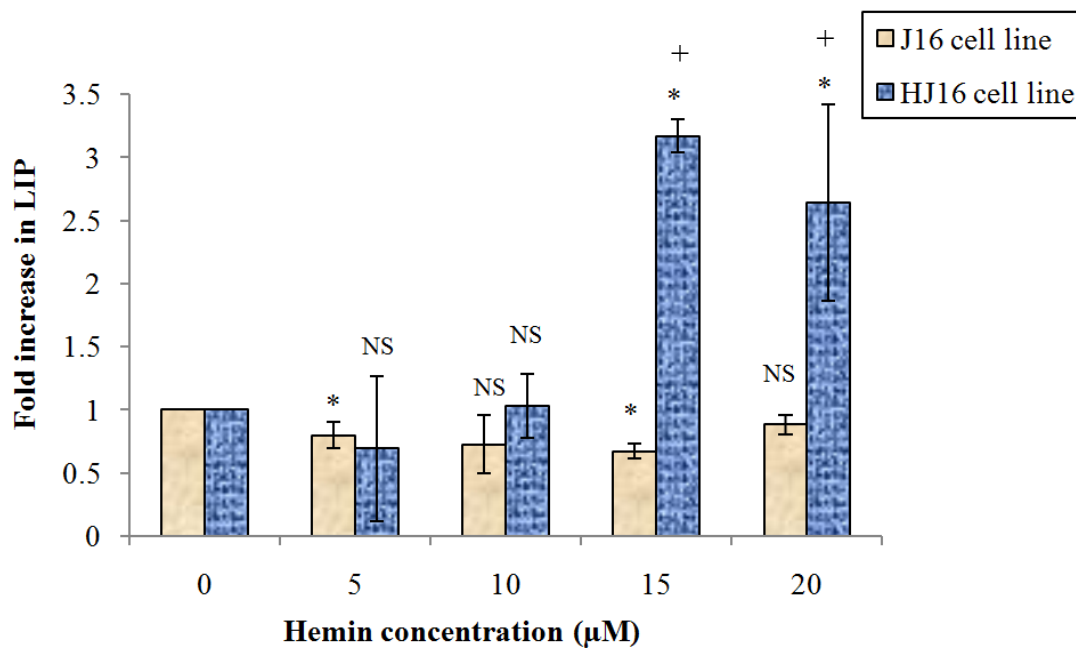


Figure 3.16:

Fold increase in LIP measurements after various concentrations of hemin.

LIP measurements were taken after J16 cell line and HJ16 cell line were treated with different concentration of hemin (i.e. 5, 10, 15, and 20 μM) for 18 h. These results are expressed as mean ± standard deviation (n=3).

* : $p < 0.05$ significant difference between untreated and treated cells.

NS : Non-significant difference between untreated and treated cells.

+ : $p < 0.05$ significant difference from the corresponding J16 cell line.

The results (see figure 3.17) showed that, in agreement with our hypothesis, in both cell lines, DFO treatment of cells pre-treated with hemin significantly decreased the levels of H₂O₂-induced necrotic cell death when compared to cells treated with hemin alone.

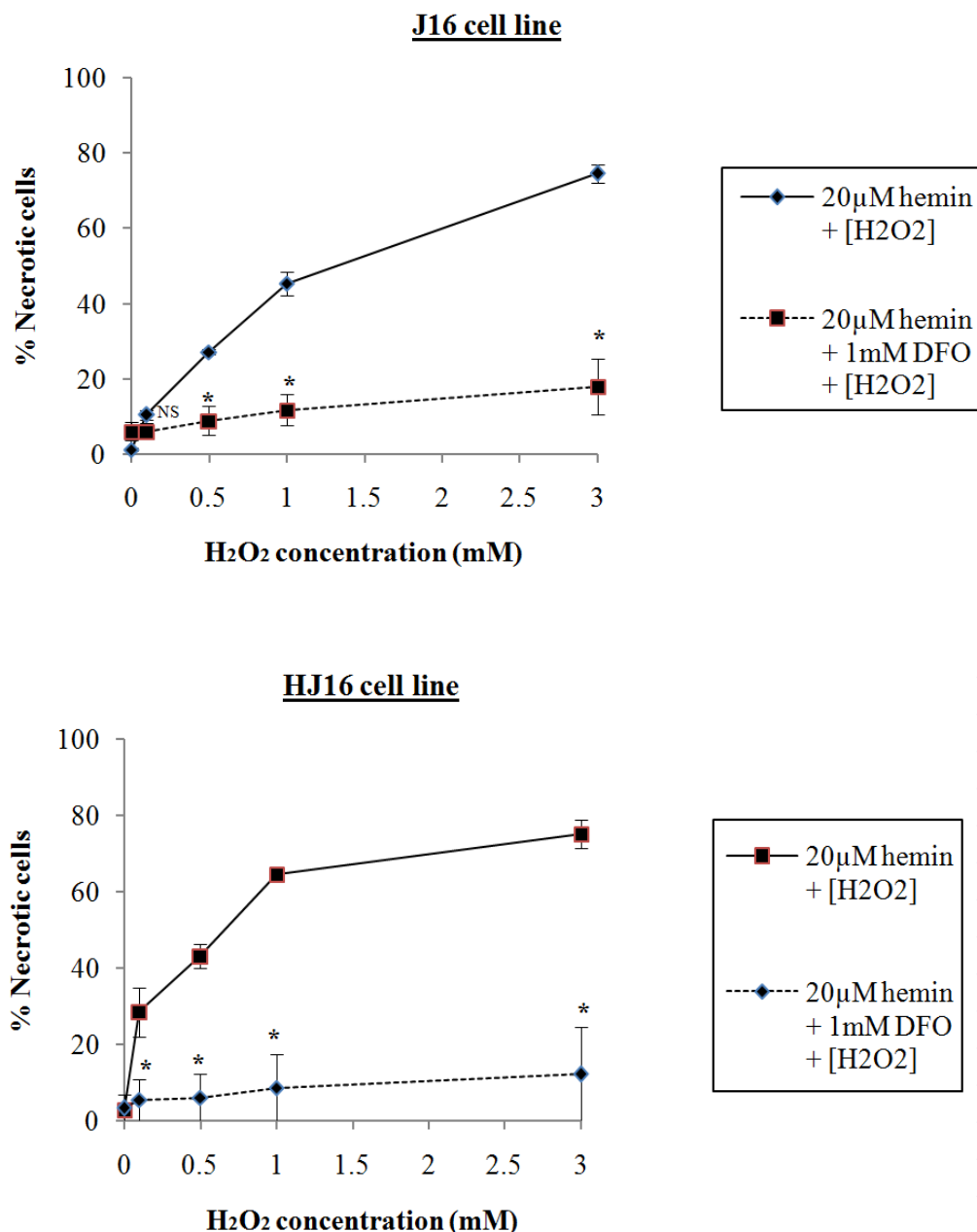
The source of iron in HJ16 cells following hemin treatment

The source of iron after overnight hemin treatment of the HJ16 cell line was an interesting point to investigate in this study. Hemin (ferric haem) is a known substrate of HO proteins (i.e. HO-1 and HO-2). Both the inducible form HO-1 and the constitutive HO-2 enzymes break down haem to release its iron (see section 1.4.2.4). This iron is then stored within the iron storage protein ferritin (Ft).

We hypothesised that the high accumulation of labile iron in HJ16 cells following hemin treatment could either be due to higher HO protein levels or lower intracellular Ft levels in HJ16 cells when compared to parental J16 cells. We therefore investigated the level of these proteins in both J16 and HJ16 cells following various treatments as detailed below.

3.4.2 The expression of HO-1 and HO-2 in Jurkat T cell lines

The higher expression of HO-1 and/or HO-2 in HJ16 cell line might contribute to accumulation of labile iron following hemin treatment. Previous analysis of the level of *ho-1* mRNA accumulation in J16 and HJ16 cells using the real-time PCR technique (Yiakouvaki, 2003) revealed that the basal level of *ho-1* cDNA is 2-fold higher in the H₂O₂-resistant HJ16 cells than in the parental J16 cells. Yiakouvaki (2003) also performed a series of Western blot analyses using a polyclonal HO-1 antibody. These Western blot analyses were not conclusive since the polyclonal antibody cross-reacted with a number of proteins in cell extracts resulting in high background and multiple bands that made the interpretation of results difficult. The study therefore moved on to use flow cytometry as a more trustworthy technique to study the expression of HO-1 in the Jurkat cells using a monoclonal antibody. The results revealed that in agreement with real-time PCR data, the basal level of HO-1 protein in H₂O₂ resistant cells was up to 2-fold higher than in parental cells.

**Figure 3.17:**

The evaluation of the susceptibility of J16 and HJ16 cell lines after DFO treatment following iron loading prior to H₂O₂ treatment.

Cells were pretreated with either 20 µM Hemin for 18 h or 20 µM Hemin for 18 h and then 1mM DFO for 2 h before H₂O₂ treatment. Flow cytometric analysis (see section 2.5) was performed 24 h after H₂O₂ treatment following dual Annexin-V/PI staining. These results are expressed as mean ± standard deviation (n=3).

* : $p < 0.05$ significantly different between the hemin (+H₂O₂) treated cells.

NS: non-significantly different when compared with the hemin (+H₂O₂) treated cells.

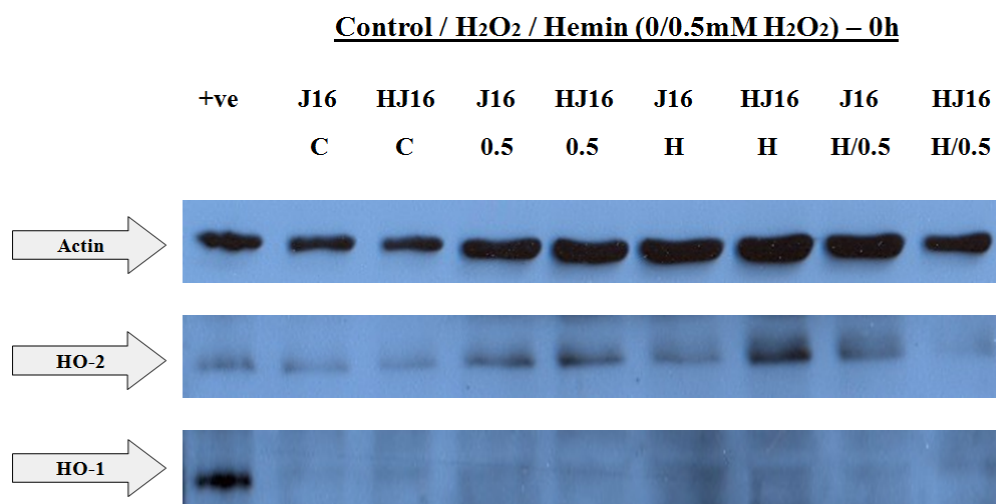
So it was concluded, with the previous observations, that HO-1 expression should play a role in hemin-induced iron accumulation in HJ16 cells. Furthermore when both cell lines were treated with 20 μ M hemin at various time points, a significant increase in HO-1 was only observed in the parental J16 cell line. Yiakouvaki (2003) concluded that HO-1 protein is not inducible in HJ16 cells presumably because gradual adaptation of cells to H₂O₂ has provoked a refractory response of HO-1 to hemin.

Since hemin is also a known substrate of HO-2 protein, it was important to check the level of its expression in Jurkat T cells. We therefore decided to carry out an in depth study of the expression of HO-1 and HO-2 at protein levels using Western blot analysis. For HO-2 analysis, we used the polyclonal antibody raised in R.M. Tyrrell's laboratory (Pourzand *et al*, 1999 and Kvam *et al*, 2000) as this antibody, unlike commercially available HO-2 antibodies, is known to be very specific. For HO-1, the Western blotting was carried out with a monoclonal antibody to avoid high background and cross-hybridisations. This antibody induced less background but still some cross hybridization was observed in the study. As a result one important positive control was added in each blot to identify the true HO-1 band in blots. That control was FEK4 cells (human fibroblast cell line) treated with a UVA dose of 250 kJ/m² and incubated in condition media (CM) for 8 h before it was collected.

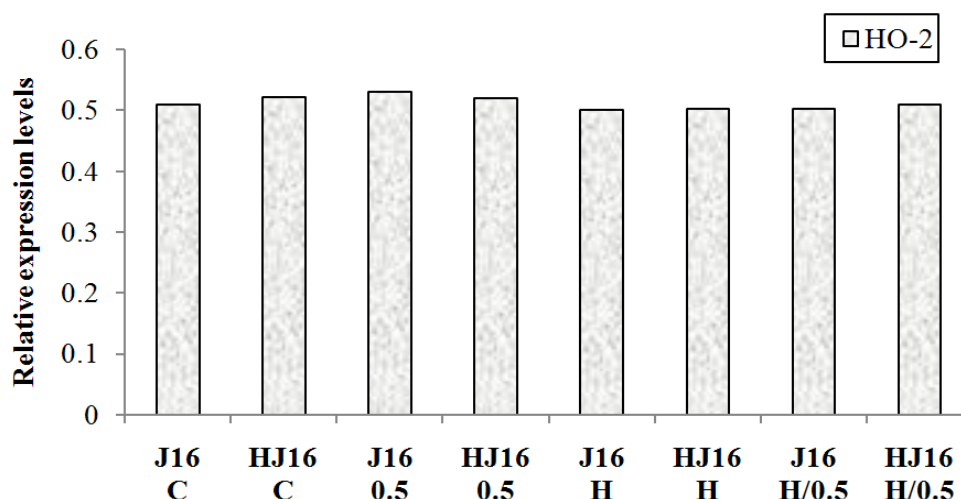
Figures 3.18 to 3.21 compare the level of HO-1 and HO-2 in both J16 and HJ16 cells collected *immediately* (0 h) or left in CM for 24 h (24 h) following hemin, DFO and/or H₂O₂ treatment. As can be seen, the basal level of HO-1 was very low in these cells and the difference in expression observed by Flow cytometry could not be visualized here. Furthermore neither overnight treatments with 20 μ M hemin, 100 μ M DFO, nor exposure to 0.5 mM H₂O₂ alone or combined with hemin or DFO treatment increased the level of HO-1 in these cell lines. The basal HO-2 level on the other hand was higher than HO-1 in both cell lines but it was not modulated by any of the above treatments.

To ascertain that HO protein levels were not modulated following hemin and/or H₂O₂, the HO-1 and HO-2 levels were followed in time course analysis from 0 to 18 and/or 24 h following hemin and/or H₂O₂ treatments. The results (see figures 3.22-3.27) revealed that neither HO-1 nor HO-2 levels are modulated by these treatments.

A.



B.

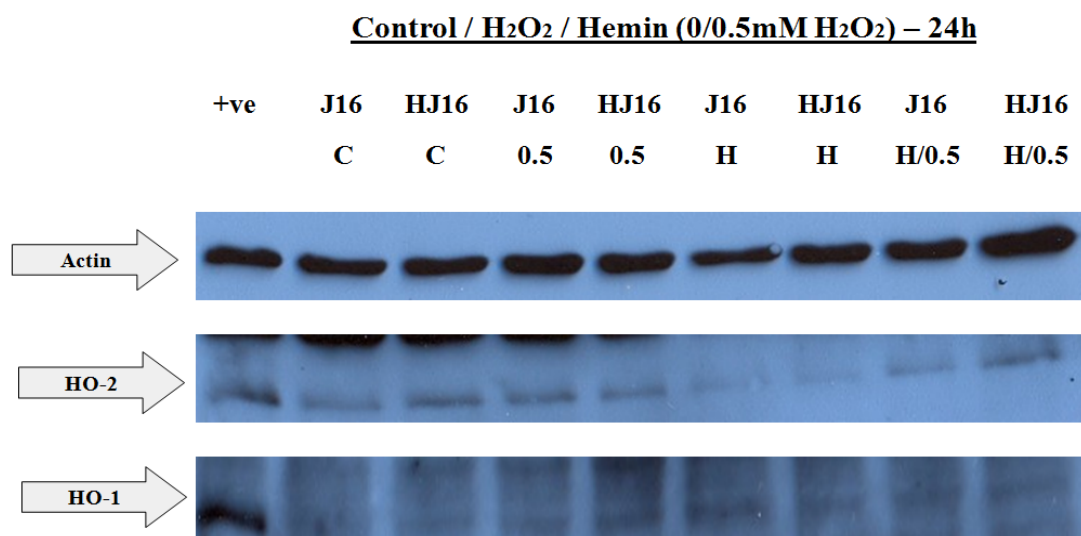
**Figure 3.18:**

The induction of HO-1 and HO-2 in J16 and HJ16 cell lines (0 h).

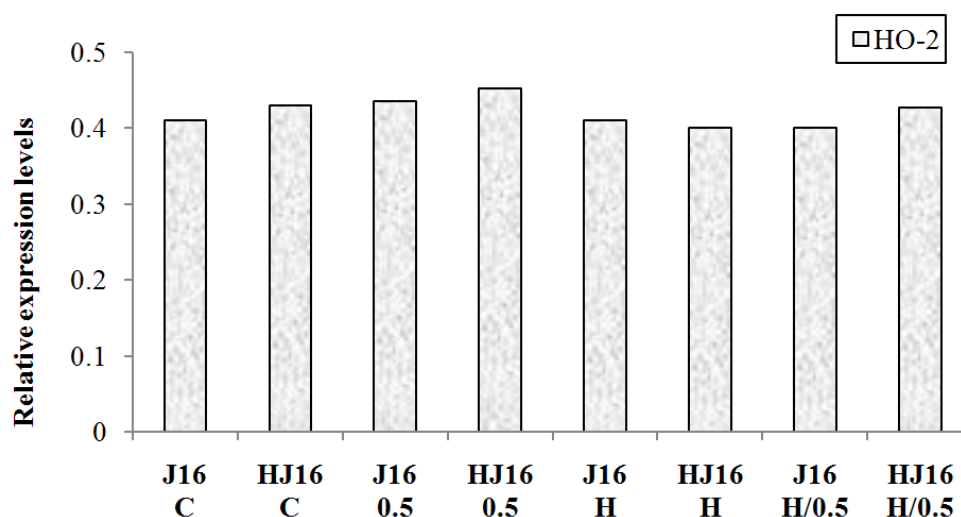
J16 and HJ16 (C) are the untreated cells (controls), J16 and HJ16 (0.5) are cells treated with 0.5mM H₂O₂, J16 and HJ16 (H) are cells treated with 20 μ M hemin for 18 h, and J16 and HJ16 (H/0.5) are cells treated overnight with 20 μ M hemin and then with 0.5mM H₂O₂. Cells were collected *immediately* following the specified treatments and used to prepare whole cellular extracts for Western blot analysis (see section 2.9). The positive control (+ve) was FEK4 cells (human fibroblast cell line) treated with a UVA dose of 250 kJ/m² and collected after 8 h. (B) The relative expression levels of HO-2 were normalised with respect to the intensity of the actin signal.

The intensities of the bands were assessed using LabImage software - Version 2.7.2 (Kapelan Bio-Imaging Solutions, Germany).

A.



B.

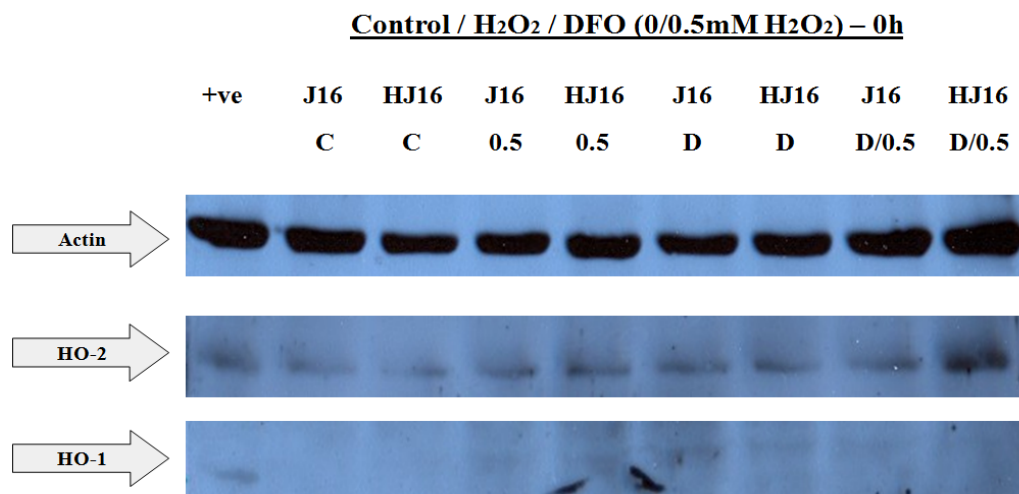
**Figure 3.19:**

The induction of HO-1 and HO-2 in J16 and HJ16 cell lines (24 h).

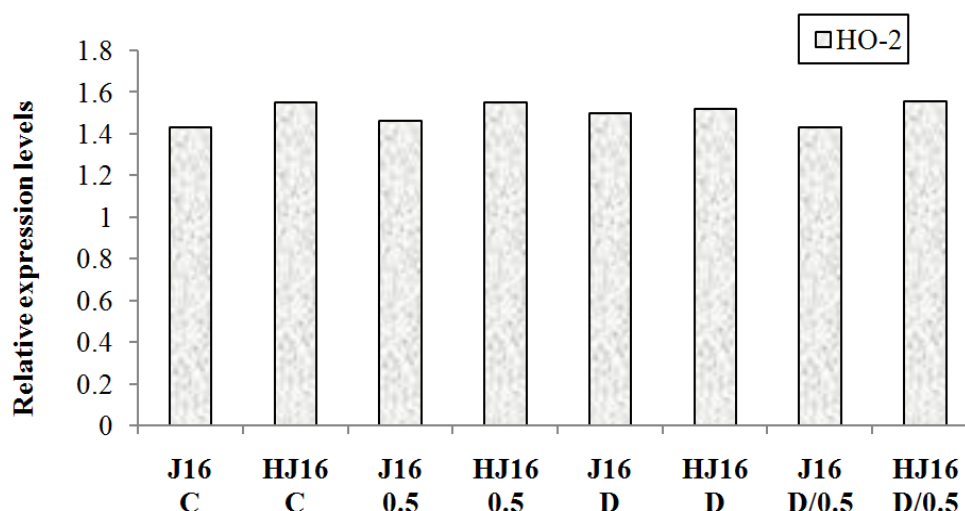
J16 and HJ16 (C) are the untreated cells (controls), J16 and HJ16 (0.5) are cells treated with 0.5mM H₂O₂, J16 and HJ16 (H) are cells treated with 20 μ M hemin for 18 h, and J16 and HJ16 (H/0.5) are cells treated overnight with 20 μ M hemin and then with 0.5mM H₂O₂. Cells were collected 24 h following the specified treatments and used to prepare whole cellular extracts for Western blot analysis (see section 2.9). The positive control (+ve) was FEK4 cells (human fibroblast cell line) treated with a UVA dose of 250 kJ/m² and collected after 8 h. (B) The relative expression levels of HO-2 were normalised with respect to the intensity of the actin signal.

The intensities of the bands were assessed using LabImage software - Version 2.7.2 (Kapelan Bio-Imaging Solutions, Germany).

A.



B.

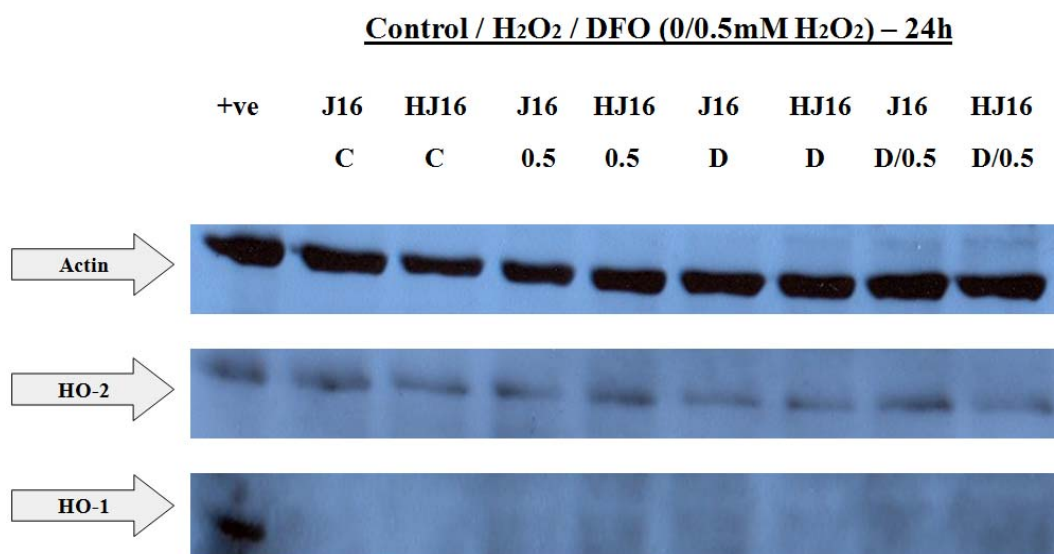
**Figure 3.20:**

The induction of HO-1 and HO-2 in J16 and HJ16 cell lines (0 h).

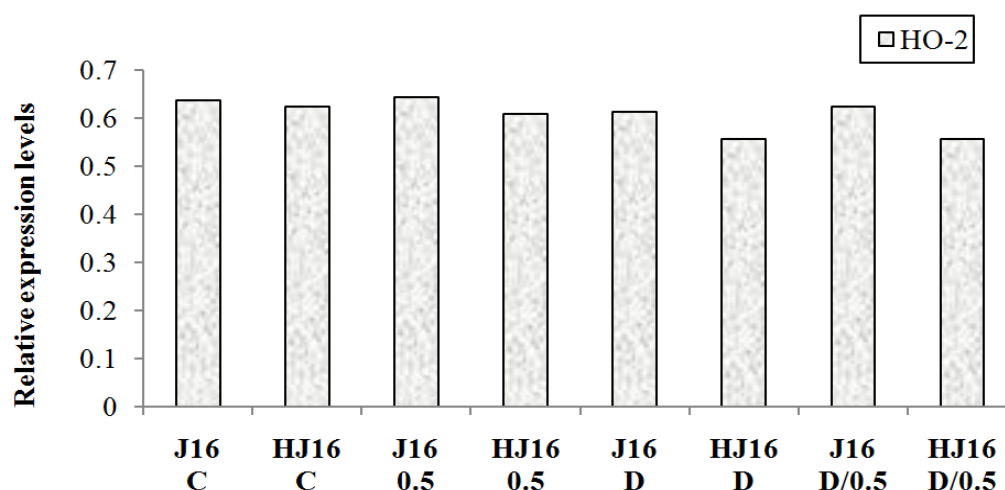
J16 and HJ16 (C) are the untreated cells (controls), J16 and HJ16 (0.5) are cells treated with 0.5mM H₂O₂, J16 and HJ16 (D) are cells treated with 100 μ M DFO for 18 h, and J16 and HJ16 (D/0.5) are cells treated overnight with 100 μ M DFO and then with 0.5mM H₂O₂. Cells were collected *immediately* following the specified treatments and used to prepare whole cellular extracts for Western blot analysis (see section 2.9). The positive control (+ve) was FEK4 cells (human fibroblast cell line) treated with a UVA dose of 250 kJ/m² and collected after 8 h. (B) The relative expression levels of HO-2 were normalised with respect to the intensity of the actin signal.

The intensities of the bands were assessed using LabImage software - Version 2.7.2 (Kapelan Bio-Imaging Solutions, Germany).

A.



B.

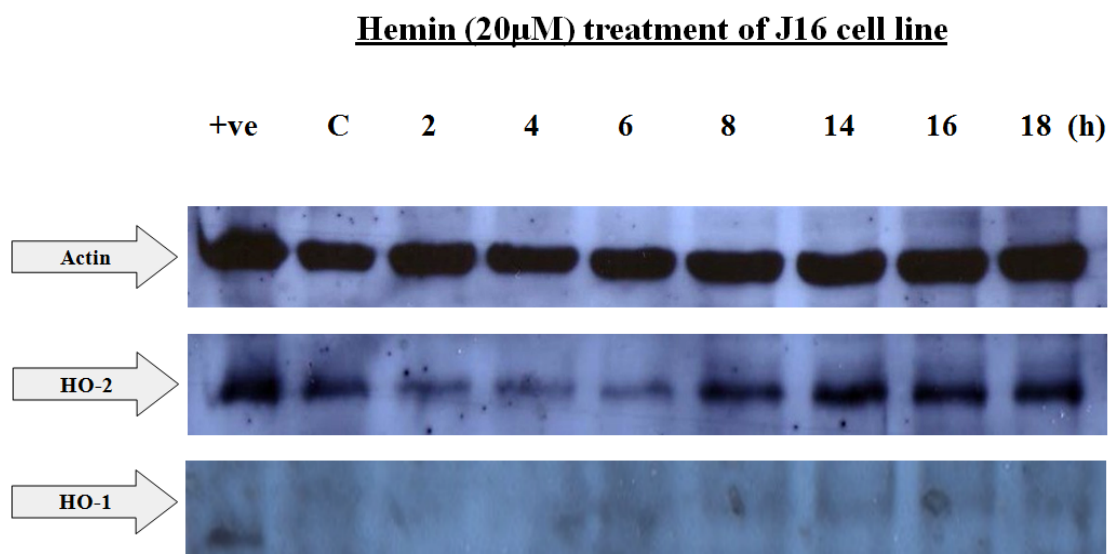
**Figure 3.21:**

The induction of HO-1 and HO-2 in J16 and HJ16 cell lines (24 h).

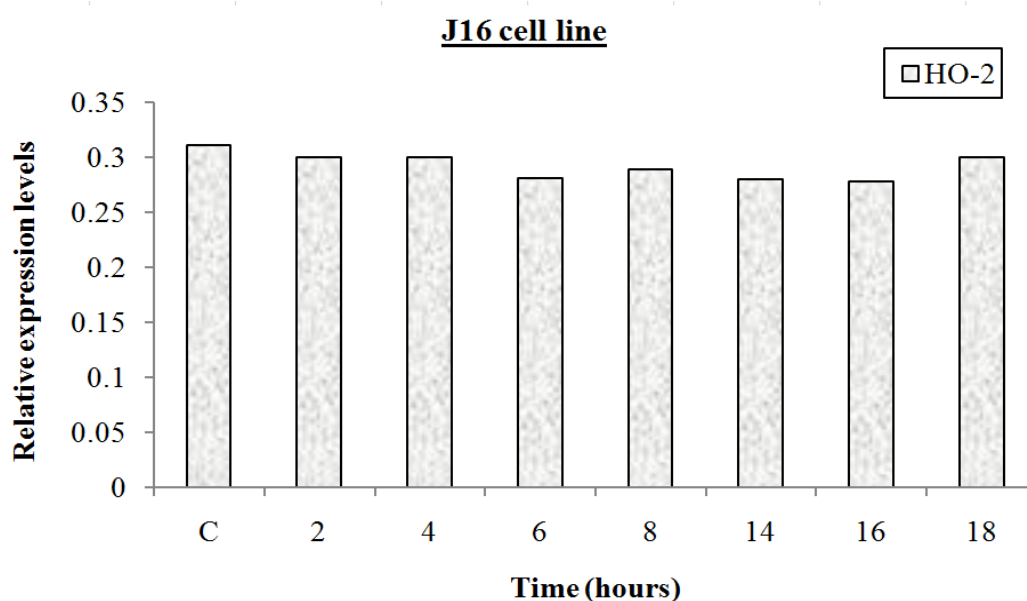
J16 and HJ16 (C) are the untreated cells (controls), J16 and HJ16 (0.5) are cells treated with 0.5mM H₂O₂, J16 and HJ16 (D) are cells treated with 100 µM DFO for 18 h, and J16 and HJ16 (D/0.5) are cells treated overnight with 100 µM DFO and then with 0.5mM H₂O₂. Cells were collected 24 h following the specified treatments and used to prepare whole cellular extracts for Western blot analysis (see section 2.9). The positive control (+ve) was FEK4 cells (human fibroblast cell line) treated with a UVA dose of 250 kJ/m² and collected after 8 h. (B) The relative expression levels of HO-2 were normalised with respect to the intensity of the actin signal.

The intensities of the bands were assessed using LabImage software - Version 2.7.2 (Kapelan Bio-Imaging Solutions, Germany).

A.



B.

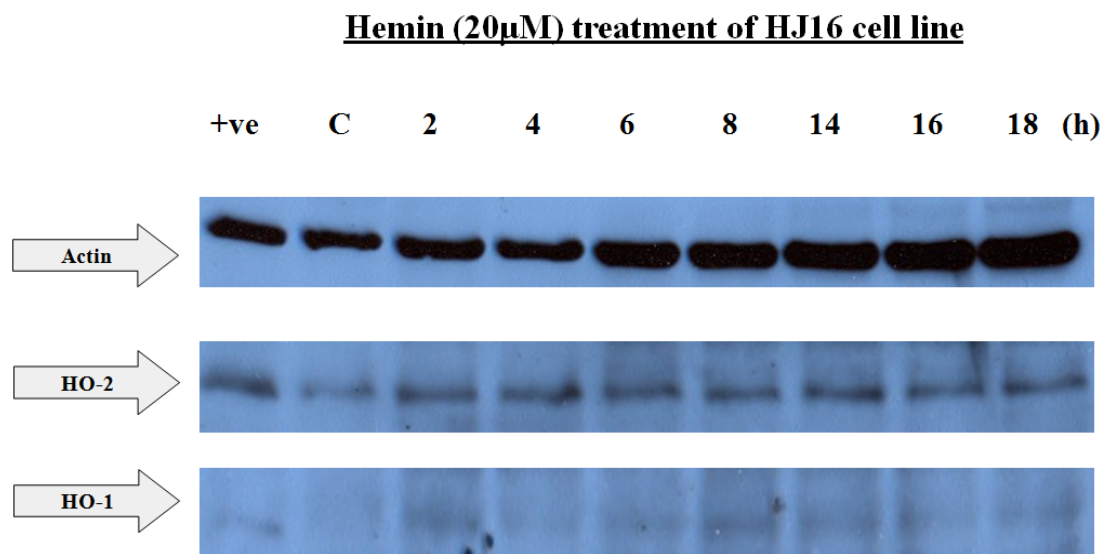
**Figure 3.22 :**

Time course induction of HO-1 and HO-2 in J16 cell line after 20 μ M hemin.

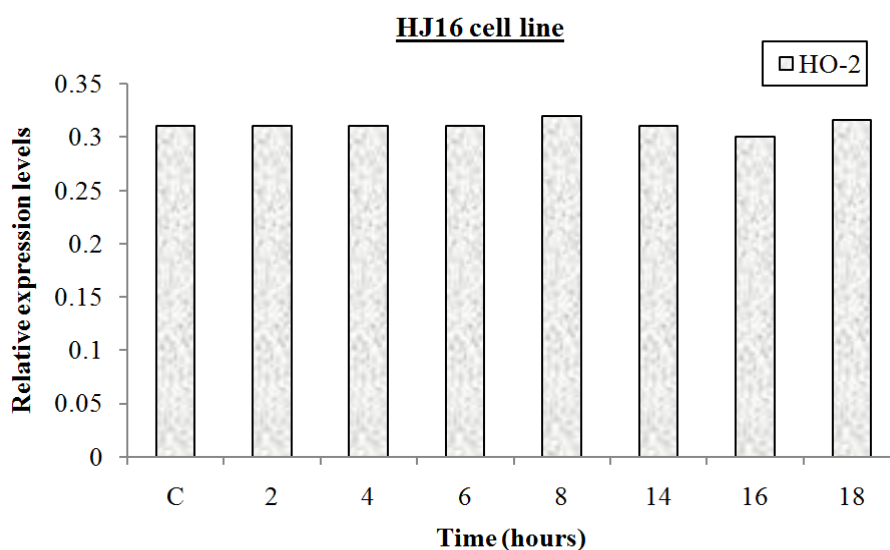
(A) J16 cell line was treated with 20 μ M hemin. Cells were collected at various times (i.e. 2, 4, 6, 8, 14, 16, and 18 h) and used to prepare whole cellular extracts for Western blot analysis (see section 2.9). The positive control (+ve) was FEK4 cells (human fibroblast cell line) treated with a UVA dose of 250 kJ/m² and collected after 8 h. (B) The relative expression levels of HO-2 were normalised with respect to the intensity of the actin signal.

The intensities of the bands were assessed using LabImage software - Version 2.7.2 (Kapelan Bio-Imaging Solutions, Germany).

A.



B.

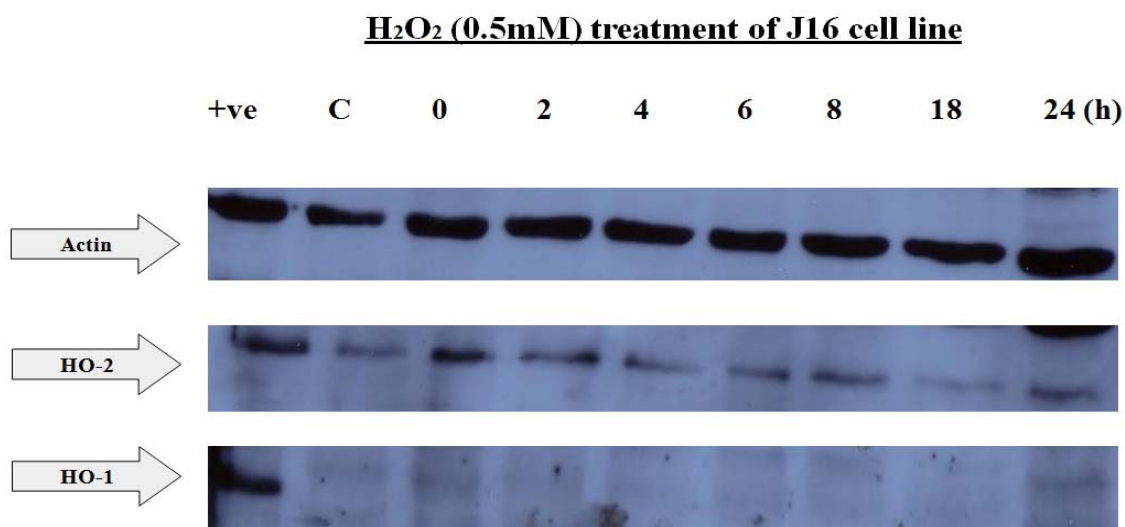
**Figure 3.23 :**

Time course induction of HO-1 and HO-2 in HJ16 cell line after 20 μ M hemin.

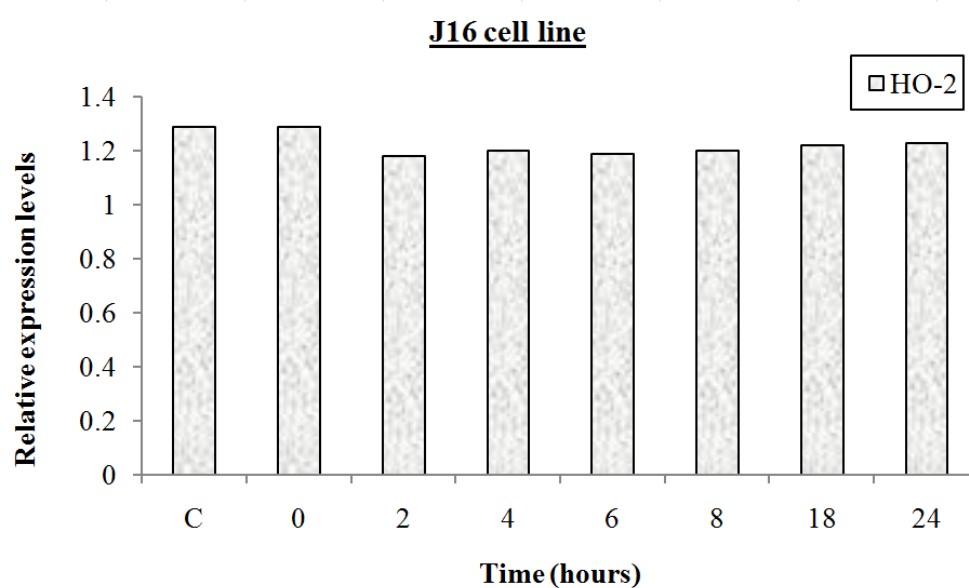
(A) HJ16 cell line was treated with 20 μ M hemin. Cells were collected at various times (i.e. 2, 4, 6, 8, 14, 16, and 18 h) and used to prepare whole cellular extracts for Western blot analysis (see section 2.9). The positive control (+ve) was FEK4 cells (human fibroblast cell line) treated with a UVA dose of 250 kJ/m^2 and collected after 8 h. (B) The relative expression levels of HO-2 were normalised with respect to the intensity of the actin signal.

The intensities of the bands were assessed using LabImage software - Version 2.7.2 (Kapelan Bio-Imaging Solutions, Germany).

A.



B.

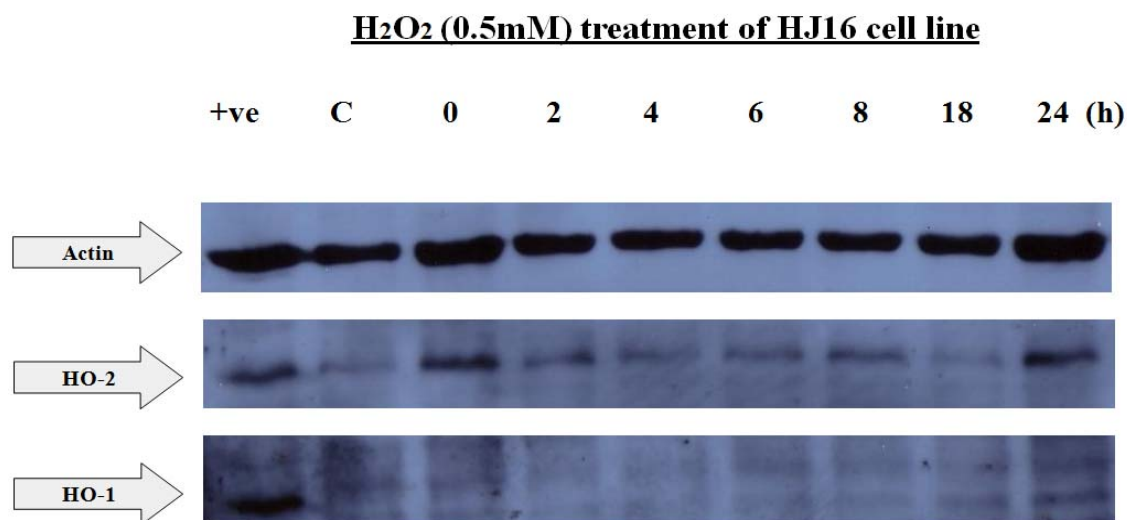
**Figure 3.24 :**

Time course induction of HO-1 and HO-2 in J16 cell line after 0.5 mM H₂O₂.

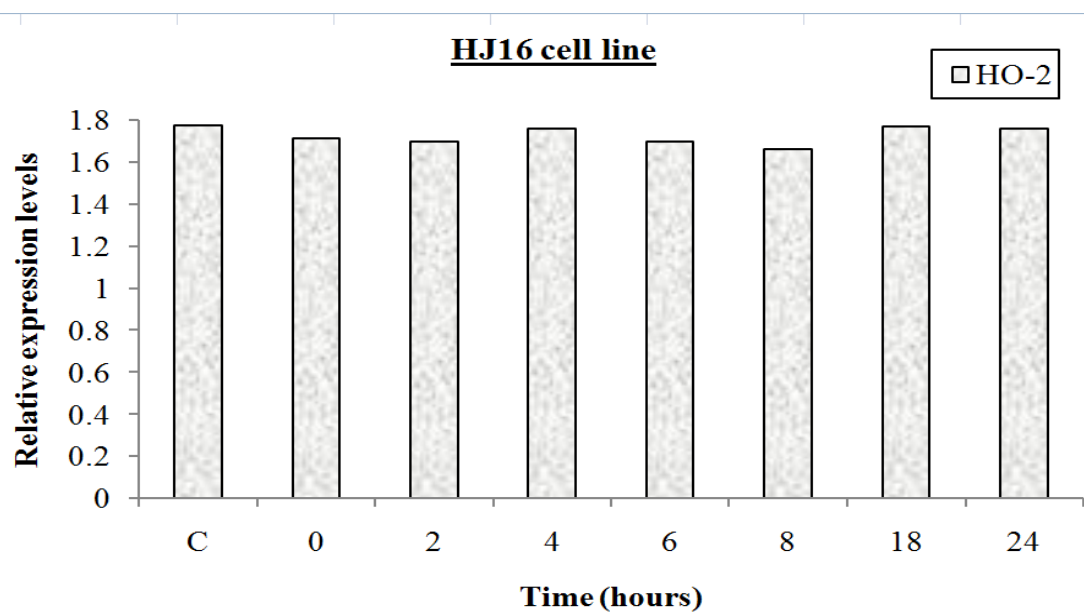
(A) J16 cell line was treated with an intermediate dose of H₂O₂ (i.e. 0.5 mM). Cells were collected at various times (i.e. 0, 2, 4, 6, 8, 18, and 24 h) and used to prepare whole cellular extracts for Western blot analysis (see section 2.9). The positive control (+ve) was FEK4 cells (human fibroblast cell line) treated with a UVA dose of 250 kJ/m² and collected after 8 h. (B) The relative expression levels of HO-2 were normalised with respect to the intensity of the actin signal.

The intensities of the bands were assessed using LabImage software - Version 2.7.2 (Kapelan Bio-Imaging Solutions, Germany).

A.



B.

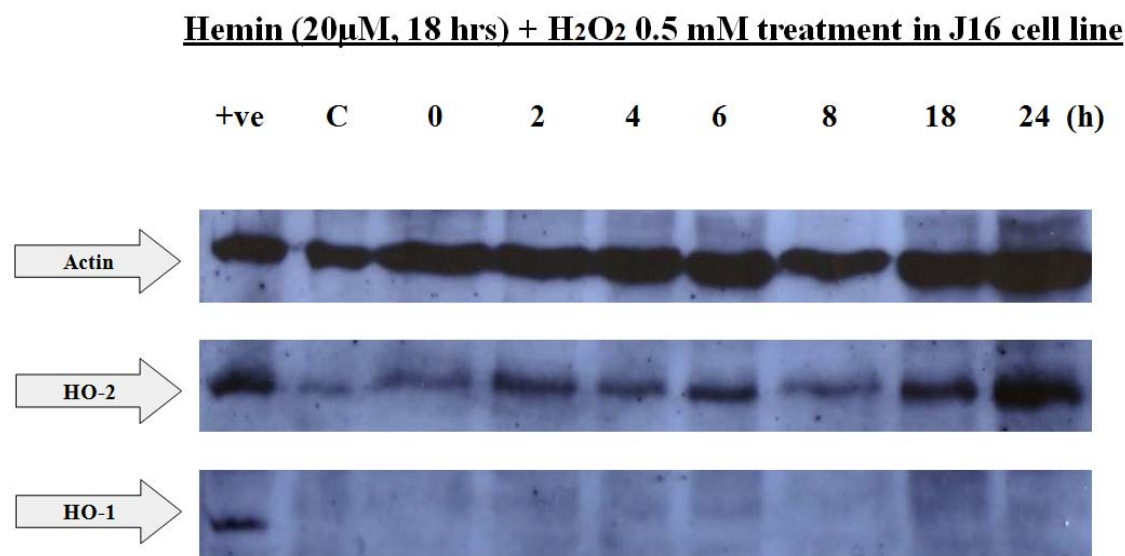
**Figure 3.25 :**

Time course induction of HO-1 and HO-2 in HJ16 cell line.

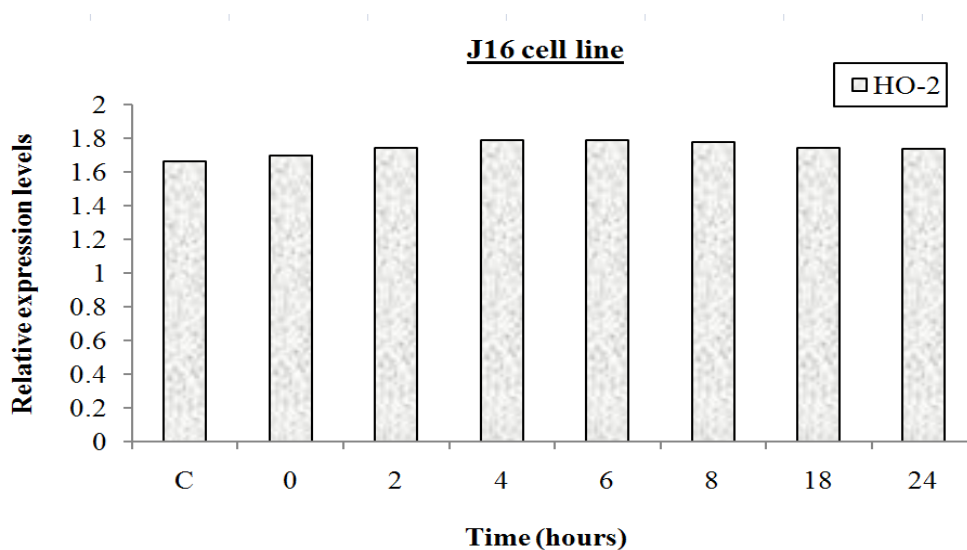
(A) HJ16 cell line was treated with an intermediate dose of H₂O₂ (i.e. 0.5 mM). Cells were collected at various times (i.e. 0, 2, 4, 6, 8, 18, and 24 h) and used to prepare whole cellular extracts for Western blot analysis (see section 2.9). The positive control (+ve) was FEK4 cells (human fibroblast cell line) treated with a UVA dose of 250 kJ/m² and collected after 8 h. (B) The relative expression levels of HO-2 were normalised with respect to the intensity of the actin signal.

The intensities of the bands were assessed using LabImage software - Version 2.7.2 (Kapelan Bio-Imaging Solutions, Germany).

A.



B.

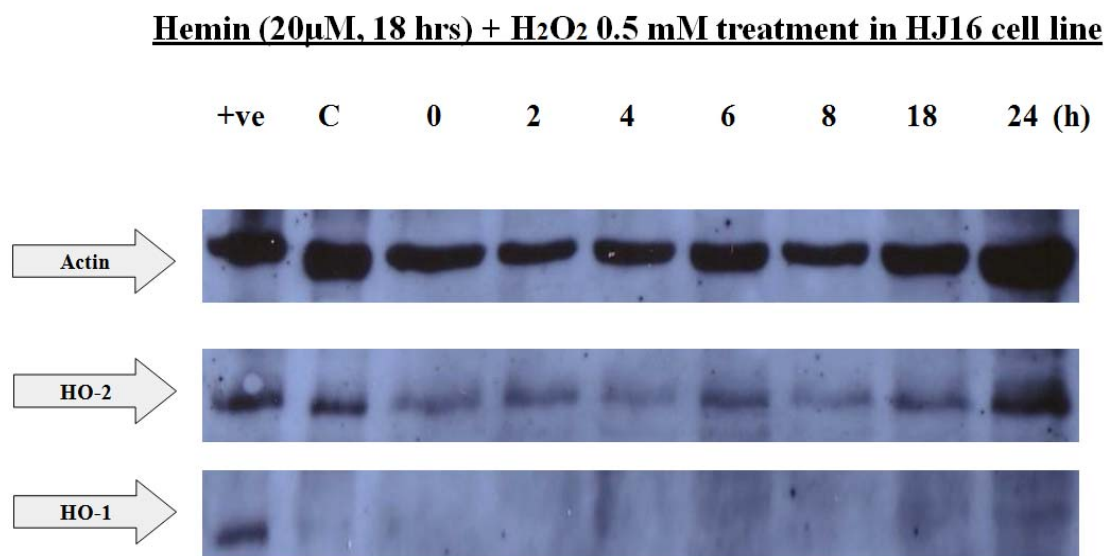
**Figure 3.26 :**

Time course induction of HO-1 and HO-2 in J16 cell line following overnight treatment of 20 μ M hemin followed by an intermediate dose of H₂O₂ (i.e. 0.5 mM)

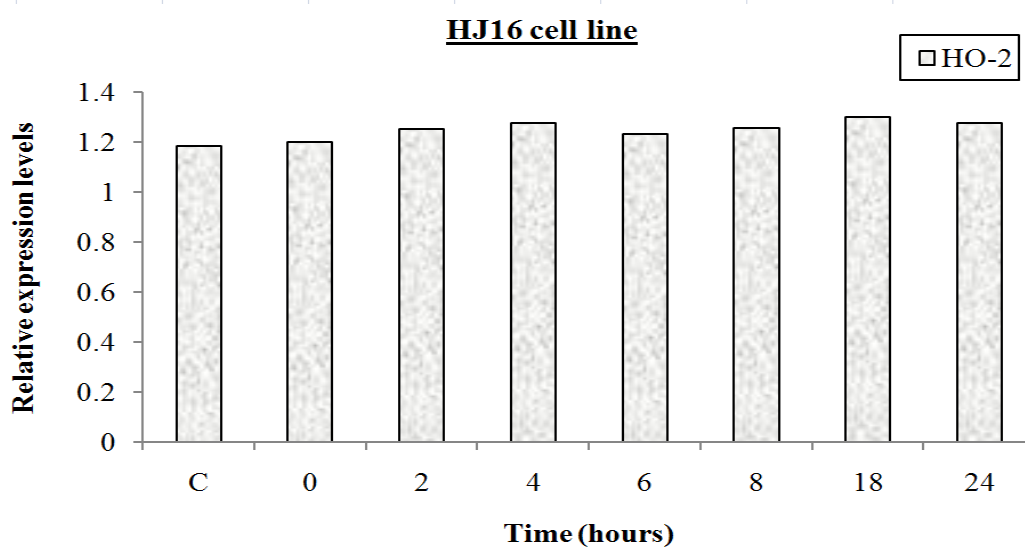
(A) J16 cell line was treated overnight with 20 μ M hemin and then with an intermediate dose of H₂O₂ (i.e. 0.5 mM). Cells were collected at various times (i.e. 0, 2, 4, 6, 8, 18, and 24 h) and used to prepare whole cellular extracts for Western blot analysis (see section 2.9). The positive control (+ve) was FEK4 cells (human fibroblast cell line) treated with a UVA dose of 250 kJ/m² and collected after 8 h. (B) The relative expression levels of HO-2 were normalised with respect to the intensity of the actin signal.

The intensities of the bands were assessed using LabImage software - Version 2.7.2 (Kapelan Bio-Imaging Solutions, Germany).

A.



B.

**Figure 3.27:**

Time course induction of HO-1 and HO-2 in HJ16 cell line following overnight treatment of 20 μ M hemin followed by an intermediate dose of H₂O₂ (i.e. 0.5 mM)

(A) HJ16 cell line was treated overnight with 20 μ M hemin and then with an intermediate dose of H₂O₂ (i.e. 0.5 mM). Cells were collected at various times (i.e. 0, 2, 4, 6, 8, 18, and 24 h) and used to prepare whole cellular extracts for Western blot analysis (see section 2.9). The positive control (+ve) was FEK4 cells (human fibroblast cell line) treated with a UVA dose of 250 kJ/m² and collected after 8 h. (B) The relative expression levels of HO-2 were normalised with respect to the intensity of the actin signal.

The intensities of the bands were assessed using LabImage software - Version 2.7.2 (Kapelan Bio-Imaging Solutions, Germany).

To complete the analysis, the level of HO-1 and HO-2 proteins were also checked after combined hemin (20 mM, 18 h) + DFO (1 mM, 2 h) and/or H₂O₂ (0.5 mM) treatment. Again here, no modulation in protein levels of HO-1 and HO-2 was observed (see figure 3.28). In summary, HO-1 expression was found to be very low and it was not induced with any of the above treatments (in both cell lines). On the other hand, HO-2 protein was present at higher levels than HO-1 in both cell lines but was not induced by any treatment used. Taken together these results showed that high iron accumulation after hemin treatment in HJ16 cells might not be related to differential expression of HO proteins in these cells.

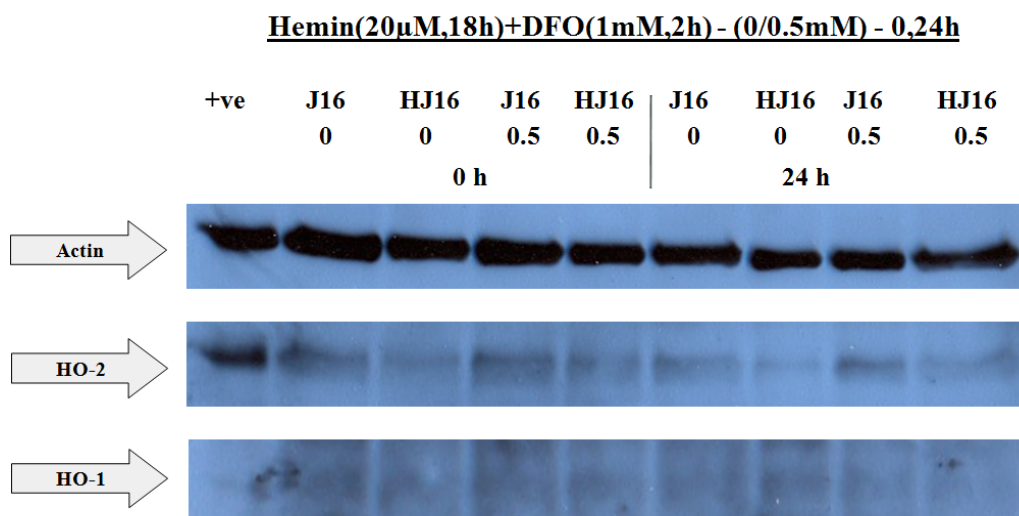
3.4.3 The level of ferritin in Jurkat T cell lines

Ferritin sequesters the potentially harmful labile iron within its shells by H-Ft's ferroxidase activity so that iron can be stored in an inactive form. Several cellular studies have shown that in oxidative stress conditions Ft may have a protective effect against oxidative damage as it removes iron that acts as a catalyst in biological oxidation (reviewed in Arosio and Levi, 2002 and Torti and Torti, 2002).

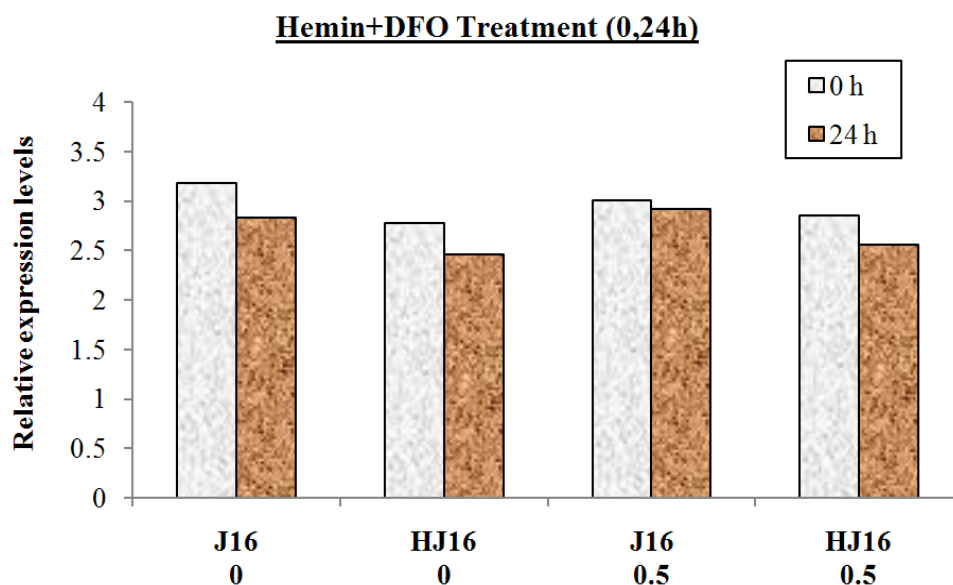
In the case of UVA irradiation however, Ft when degraded has been identified as a potential source of harmful labile iron that triggers necrotic cell death in skin fibroblasts (Pourzand *et al*, 1999). Indeed UVA has been shown to promote the proteolytic degradation of Ft and the consequent release of potentially harmful labile iron in skin cells. The release of Ft's iron exacerbates the extent of UVA-induced peroxidative damage in the cell membrane as well as membranes of vital organelles, notably those of mitochondria and lysosomes, leading to necrotic cell death (Zhong *et al*, 2004). The proteolytic degradation of Ft occurs as a result of damage to lysosomal membranes leading to leakage of potentially harmful lysosomal proteases into the cytosol which in turn act to degrade cytosolic proteins, notably Ft.

Studies by Brunk and co-workers (Brunk *et al*, 1995^b) have demonstrated that acute exposure of macrophage-like J-774 cells to H₂O₂ also triggers lysosomal damage. The irradiation of human fibroblasts with a moderate dose of blue light also resulted in oxidative apoptotic cell death as a result of damage to lysosomal organelles (Brunk *et al*, 1997).

A.



B.

**Figure 3.28 :**

The induction of HO-1 and HO-2 in J16 and HJ16 cell lines (0,24 h)

(A) J16 and HJ16 (0) are cells treated with 20 μ M hemin for 18 h and then with 1 mM DFO for 2 h, and J16 and HJ16 (0.5) are cells with 20 μ M hemin for 18 h and then with 1 mM DFO for 2 h and finally with 0.5mM H_2O_2 . Cells were collected at 0 and 24 h following the specified treatments mentioned above, and used to prepare whole cellular extracts for Western blot analysis (see section 2.9). The positive control (+ve) was FEK4 cells (human fibroblast cell line) treated with a UVA dose of 250 kJ/m^2 and collected after 8 h. (B) The relative expression levels of HO-2 were normalised with respect to the intensity of the actin signal.

The intensities of the bands were assessed using LabImage software - Version 2.7.2 (Kapelan Bio-Imaging Solutions, Germany).

Damage to lysosomes was accompanied by leakage of lysosomal contents including hydrolytic enzymes, such as cathepsin D (CATH D) (Roberg and Öllinger, 1998) that should almost certainly lead to proteolytic degradation of Ft as well.

Interestingly epidermal skin keratinocytes that have low basal levels of Ft and LIP are naturally resistant to UVA-induced necrotic cell death but overnight hemin treatment renders these cells vulnerable to UVA-induced peroxidative damage and necrotic cell death (Zhong *et al*, 2004). This is because iron loading of cells with hemin increases strongly the level of intracellular Ft which in turn increases the level of UVA-induced LIP upon radiation-mediated proteolysis of Ft molecules.

Since HJ16 cells' resistance to H₂O₂ was abolished after hemin treatment presumably because of high accumulation of labile iron in these cells, it was important to investigate the role of Ft in this phenomenon. Ferritin level was first investigated by Western blot analysis (Yiakouvaki, 2003) but because the H- and L-Ft levels were not detectable, it was decided to do the analysis by ELISA that is a more sensitive assay to detect low protein levels in cellular studies. Tables 3.6 and 3.7 (a, b, c, and d), and figures 3.29-3.33 summarises the ELISA results in J16 and HJ16 cells following various treatments.

3.4.3.1 Basal levels of Ft in J16 and HJ16 cell line

As it can be seen in table 3.6-a, the 'basal' levels of H-Ft in J16 cell line (381.3 ± 53.6 ng/mg) were found to be more than 7 fold higher than in HJ16 cell line (51.6 ± 2 ng/mg). The lower H-Ft levels in HJ16 might be part of the adaptive response developed during gradual adaptation of these cells to H₂O₂. As for L-Ft they had the same 'basal' level; 10.2 ± 3 ng/mg in J16 cells and 9.2 ± 0.95 ng/mg in HJ16 cells.

3.4.3.2 Effect of H₂O₂ on the Ft levels

When cells were treated with 0.5 mM H₂O₂ and the Ft levels were measured *immediately* (see table 3.6-b) the H-Ft level decreased to 70 % of the control value in J16 cells but did not affect significantly the L-Ft. The H-Ft levels in HJ16 were not significantly affected by H₂O₂ treatment, L-Ft on the other hand increased up to 3-fold of the control value (see table 3.6-b).

Table 3.6 a: Basal H- & L-Ft measurements in J16 and HJ16 cell lines

Cell line	H-Ft (ng/mg)	%	L-Ft (ng/mg)	%
J16	381 ± 54	100	10 ± 3	100
HJ16	52 ± 2	100	9 ± 1	100

Table 3.6 b: H- & L-Ft measurements *immediately* following H₂O₂-0.5mM

Cell line	H-Ft (ng/mg)	%	L-Ft (ng/mg)	%
J16	263 ± 36	69	15 ± 6	Non-significant
HJ16	58 ± 8	Non-significant	26 ± 7	288

Table 3.6 c: H- & L-Ft measurements *immediately* following 100 µM DFO for 18 h

Cell line	H-Ft (ng/mg)	%	L-Ft (ng/mg)	%
J16	32 ± 8	8	3 ± 1	30
HJ16	20 ± 2	38	18 ± 4	200

Table 3.6 d: H- & L-Ft measurements *immediately* following 20 µM hemin for 18 h

Cell line	H-Ft (ng/mg)	%	L-Ft (ng/mg)	%
J16	965 ± 30	253	52 ± 8	520
HJ16	380 ± 11	730	20 ± 10	222

Note : H- and L-Ft measurements performed by ELISA (see section 2.10) *immediately* following the condition/treatments specified above. The percentage represents the significant difference of the corresponding basal levels. These results are expressed as mean ± standard deviation (n=3).

But when the cells were incubated for 24 h in CM following H₂O₂ treatment (see table 3.7-b), the H-Ft decreased more in J16 cells (i.e. to 32 % of the control value) but there not a significant change in HJ16 cells. The L-Ft on the other hand, was not significantly affected in J16 cells, but was increased in HJ16 cells by 2.4-fold of the control value (see table 3.7-b).

The time course experiment (see figure 3.29) further revealed that following H₂O₂ treatment the levels of H-Ft decreased gradually in J16 cells at 6 h post treatment time point and then remained low up to 24 h following treatment. Hydrogen peroxide treatment of cultured fibroblasts and macrophages significantly inhibited the synthesis of Ft (Pantopoulos and Hentze, 1995 and Mehrlhase *et al*, 2005, respectively). This is also shown when rat liver lysates were subjected to postischemic reperfusion (Tacchini *et al*, 1997). The L-Ft time course study following H₂O₂ treatment revealed that the L-Ft levels remain unchanged in J16 cells but slightly increase up to 2-fold control value in HJ16 cells at 6 h time point and then return to around control value at 24 h (see figure 3.29).

3.4.3.3 Effect of DFO ± H₂O₂ on the Ft levels

The treatment of cells with 100 µM DFO strongly reduced the level of H-Ft in J16 cells to 8 % of the control value (see table 3.6-c and figure 3.30-A1). In HJ16 cells, DFO treatment also decreased the level of H-Ft although to a lesser extent than in J16 cells (i.e. to 38 % of the control value). The decrease in H-Ft levels by DFO is consistent with previous observations showing that DFO diminishes Ft biosynthesis in B6 fibroblasts (Pantopoulos and Hentze, 1995) and reduces Ft levels in macrophages (Mehrlhase *et al*, 2005). The L-Ft levels on the other hand decreased significantly in J16 but were strongly induced in HJ16 cells (see table 3.6-b and figure 3.30-A2). Following 24 h incubation in CM after the DFO treatment (see table 3.7-c and figure 3.30-B1), H-Ft decreased significantly in J16 and HJ16 cells (i.e. to 6 % and 15 % of the control values, respectively). DFO treatment of HeLa cells demonstrated nearly a total repression of Ft (Cairo *et al*, 1985), as it also significantly decreased both subunits in K562 cells (Konijn *et al*, 1999). On the other hand, the L-Ft levels (see table 3.7-c and figure 3.30-B2) decreased significantly in J16 cells but there was a non-significant increase in HJ16 cells.

Table 3.7 a: Basal H- & L-Ft measurements in J16 and HJ16 cell lines

Cell line	H-Ft (ng/mg)	%	L-Ft (ng/mg)	%
J16	381 ± 54	100	10 ± 3	100
HJ16	52 ± 2	100	9 ± 1	100

Table 3.7 b: H- & L-Ft measurements 24 h following H₂O₂-0.5mM

Cell line	H-Ft (ng/mg)	%	L-Ft (ng/mg)	%
J16	122 ± 51	32	14 ± 6	Non-significant
HJ16	42 ± 15	Non-significant	22 ± 8	244

Table 3.7 c: H- & L-Ft measurements 24 h following 100 µM DFO for 18 h

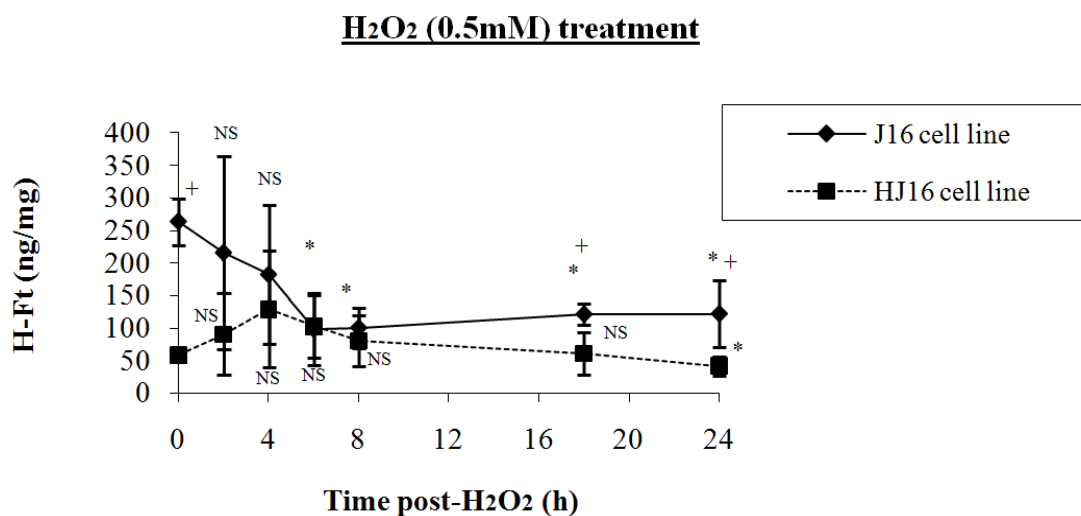
Cell line	H-Ft (ng/mg)	Fold difference	L-Ft (ng/mg)	%
J16	23 ± 14	6	2 ± 1	20
HJ16	8 ± 3	15	12 ± 3	Non-significant

Table 3.7 d: H- & L-Ft measurements 24 h following 20 µM hemin for 18 h

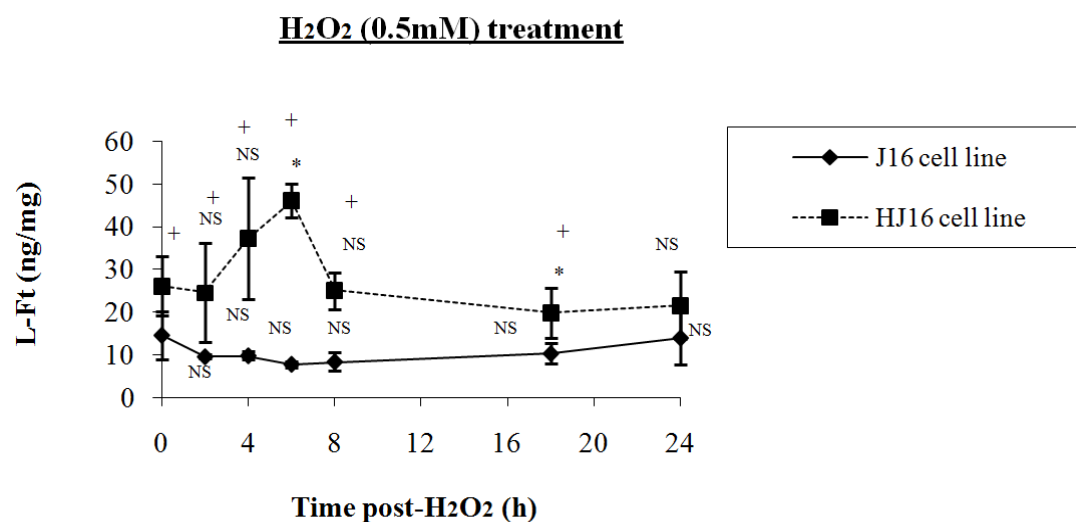
Cell line	H-Ft (ng/mg)	%	L-Ft (ng/mg)	%
J16	1443 ± 150	379	30 ± 10	300
HJ16	474 ± 49	912	69 ± 19	767

Note : H- and L-Ft measurements performed by ELISA (see section 2.10) *immediately* following the condition/treatments specified above. The percentage represents the significant difference of the corresponding basal levels. These results are expressed as mean ± standard deviation (n=3).

A.



B.

**Figure 3.29:**

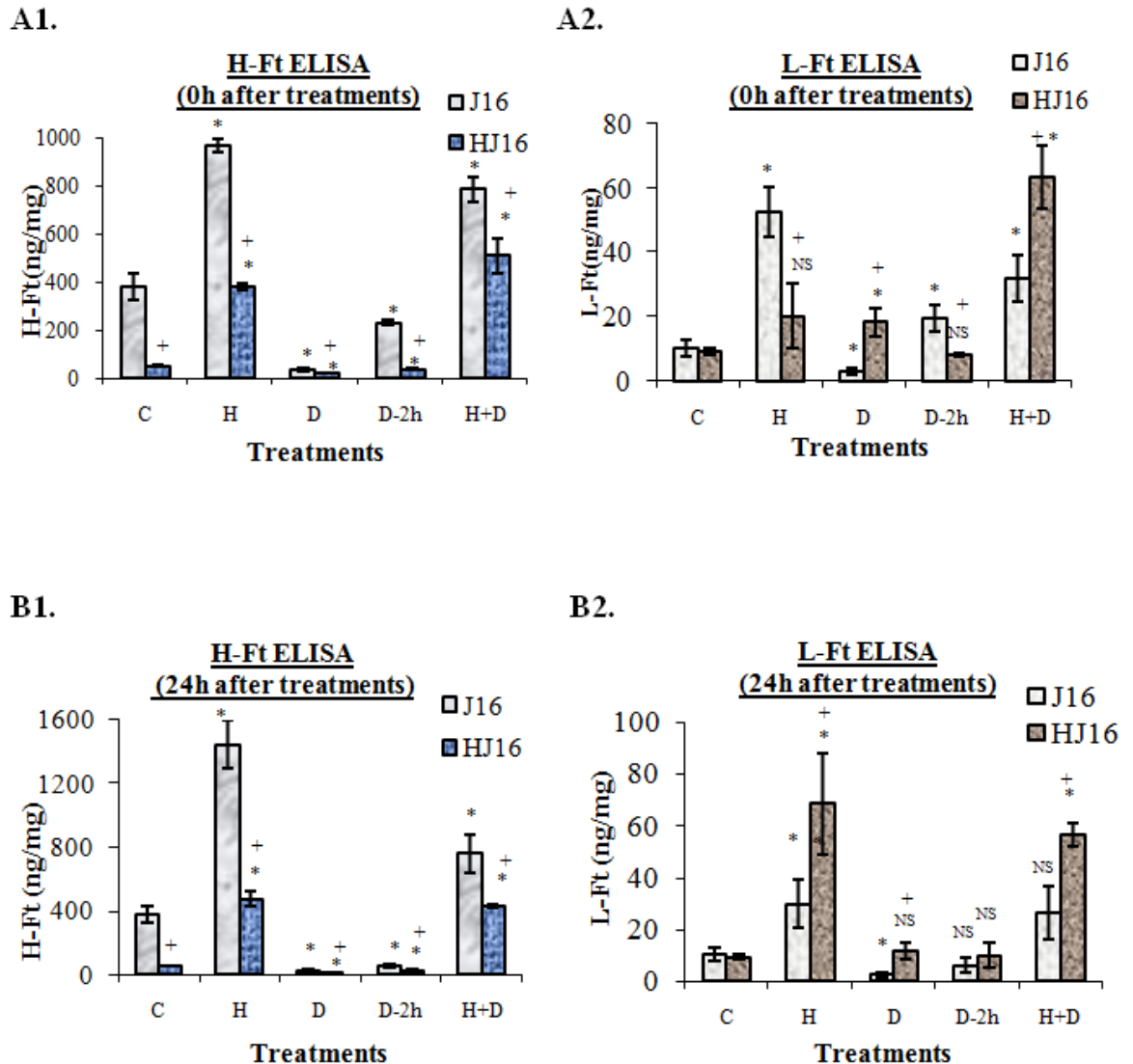
Effect of 0.5 mM H₂O₂ on H and L-Ft in J16 and HJ16 cell lines.

J16 and HJ16 cell lines were treated with an intermediate dose of H₂O₂ (i.e. 0.5 mM) and were then collected at various times (i.e. 2, 4, 6, 8, 18, and 24 h). Whole cellular extracts were prepared for Ferritin ELISA (see section 2.10) to investigate the roles of H and L-Ft (A. and B., respectively). These results are expressed as mean ± standard deviation (n=3).

* : $p < 0.05$ significant difference between corresponding control.

NS : Non-significant difference between corresponding control.

+ : $p < 0.05$ significantly different when compared with the other cell line.

**Figure 3.30:**

Effect of hemin or/and DFO on H and L-Ft in J16 and HJ16 cell lines (0,24 h).

J16 and HJ16 cell lines were either treated overnight with 20 μ M hemin (H), 100 μ M DFO (D), 1mM DFO for 2 h (D-2h), or with 20 μ M hemin for 18 h and then with 1 mM DFO for 2 h (H+D). Cells were either collected *immediately* after the specified treatment (i.e. 0h, A1 and A2) or after incubating them in CM for 24 h following the specified treatments (i.e. 24 h, B1 and B2) and used to prepare whole cellular extracts for Ferritin ELISA (see section 2.10) to investigate the roles of H and L-Ft (A1 – B1 and A2 – B2, respectively). These results are expressed as mean \pm standard deviation (n=3).

* : $p < 0.05$ significant difference between corresponding control.

NS : Non-significant difference between corresponding control.

+ : $p < 0.05$ significantly different when compared with the corresponding J16 cells.

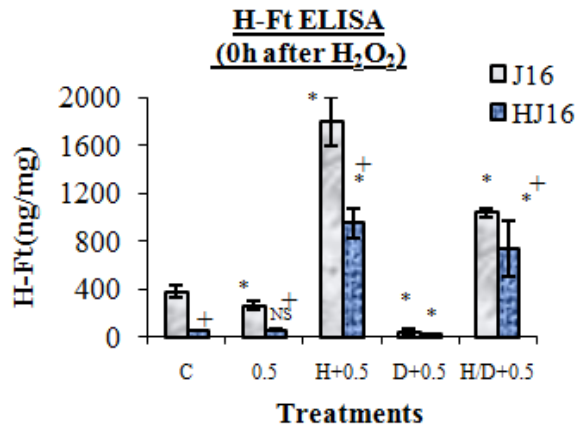
DFO treatment of cells (100 μ M, 18 h) followed by H₂O₂ treatment, decreased significantly the H-Ft in both J16 cells and HJ16 cells (i.e. to 11 % and 38 % of the control values, respectively) (see figure 3.31-A1). On the other hand, not a significant change in the L-Ft expression in both cell lines (see figure 3.31-A2). The same relationship between H- and L-Ft was also observed when cells were incubated for another 24 h in CM following DFO + H₂O₂ treatment; H-Ft was strongly decreased in both J16 cells and HJ16 cells (i.e. to 7 % and 13 % of the control values, respectively) (see figure 3.31-B1). On the other hand, there was a non-significant change in the L-Ft expression was observed in both cell lines (see figure 3.31-B2).

3.4.3.4 Effect of hemin \pm H₂O₂ on the Ft levels

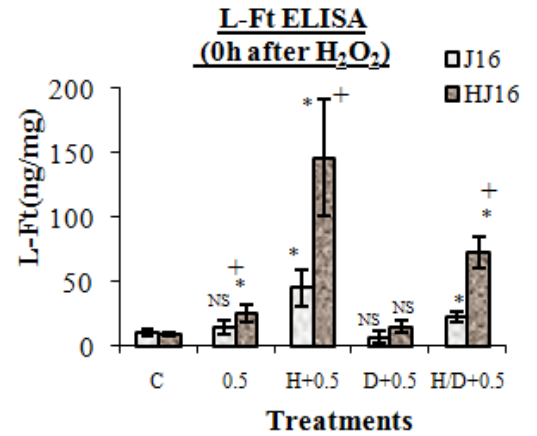
The time course experiment following hemin treatment revealed that the increase in H- or L-Ft in the J16 and HJ16 cells was not highly induced in the early hours after treatment (see figure 3.32), presumably because Ft molecules takes time to get synthesized. The latter data are expected as hemin should first be broken down by HO and release its iron which in turn will stimulate *de novo* Ft synthesis. The iron accumulation in HJ16 cells after hemin treatment is only apparent after 2 h post treatment (see table 3.5) with a peak at 6h after which it is reduced, presumably because of sequestration of a portion of it in the newly synthesized Ft molecules. This timing coincides with detection of higher Ft levels presumably as a result of its *de novo* synthesis. The H-Ft in J16 cells decreased up to 4 h and then was strongly induced after 8 h till 24 h after hemin treatment. The L-Ft, on the other hand, did not significantly increase during the time course in J16 cells, except at 18 and 24 h (see figure 3.32).

When J16 cells were treated with 20 μ M hemin for 18 h and the Ft levels were measured *immediately*, both the H-Ft and L-Ft were significantly induced (i.e. up to 2.5-fold and 5-fold of the control values, respectively) (see table 3.6-d and figure 3.30-A1,A2). In HJ16 cells, the same treatment strongly increased the levels of H-Ft (i.e. up to 7.3-fold of the control value). On the other hand, there was a non-significant change in the L-Ft expression (see table 3.6-d and figure 3.30-A1,A2). Ferritin biosynthesis also strongly increased in B6 fibroblasts pre-treated with haem arginate (Pantopoulos and Hentze, 1995).

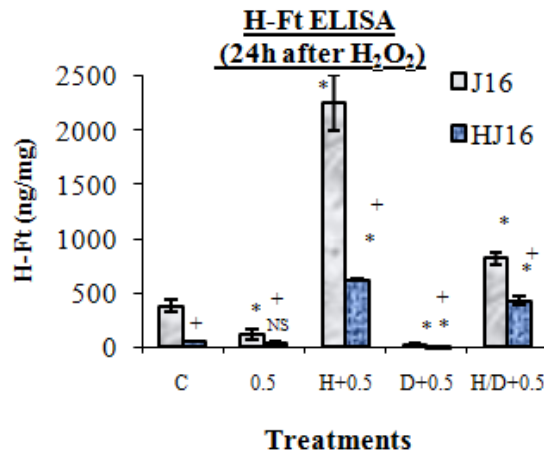
A1.



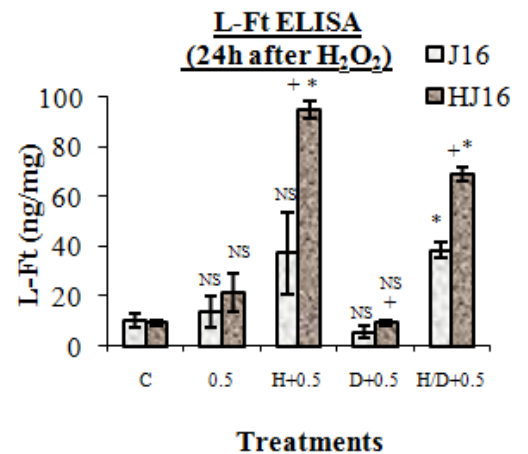
A2.



B1.



B2.

**Figure 3.31:**

Effect of hemin and/or DFO prior to H₂O₂ treatment on H and L-Ft in J16 and HJ16 cell lines (0, 24h).

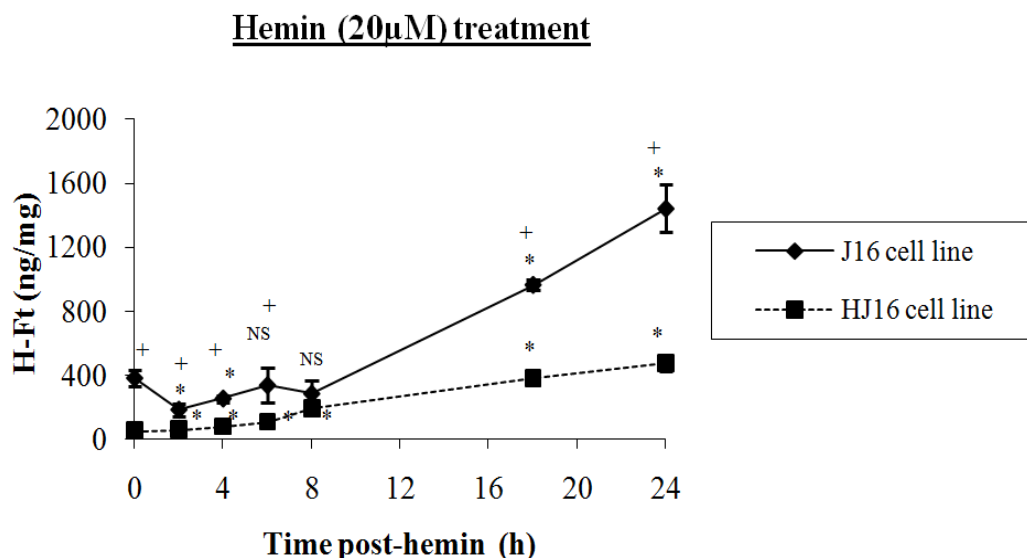
J16 and HJ16 cell lines were either treated with 0.5mM H₂O₂ alone (0.5), treated overnight with 20μM hemin and then with 0.5mM H₂O₂ (H+0.5), treated overnight with 100 μM DFO and then with 0.5mM H₂O₂ (D+0.5), or treated with 20 μM hemin for 18 h and then with 1 mM DFO for 2 h and finally with 0.5mM H₂O₂ (H/D+0.5). Cells were either collected *immediately* after the specified treatment (i.e. 0h, A1 and A2) or after incubating them in CM for 24 h following the specified treatments (i.e. 24 h, B1 and B2) and used to prepare whole cellular extracts for Ferritin ELISA (see section 2.10) to investigate the roles of H and L-Ft (A1 – B1 and A2 – B2, respectively). These results are expressed as mean ± standard deviation (n=3).

* : $p < 0.05$ significant difference between corresponding control.

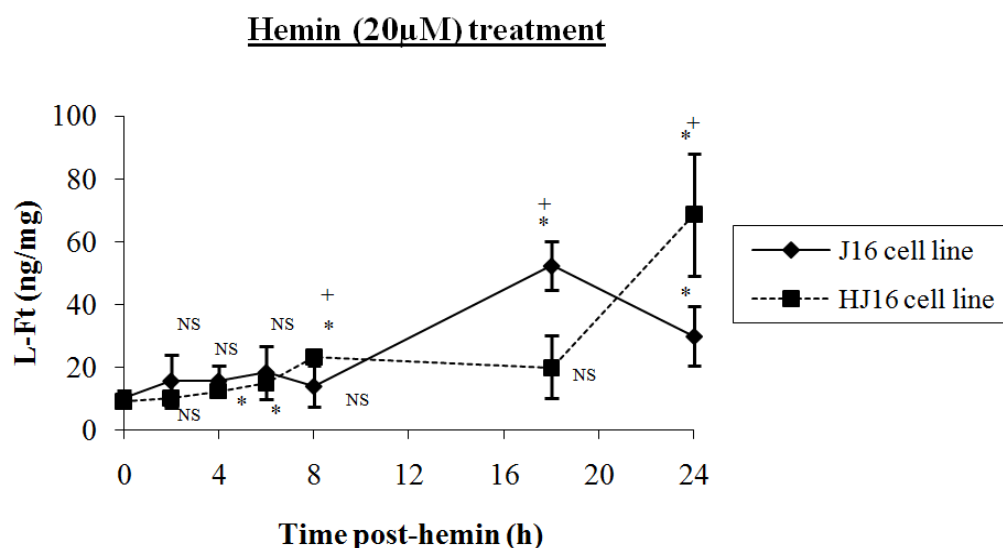
NS : Non-significant difference between corresponding control.

+ : $p < 0.05$ significantly different when compared with the corresponding J16 cells.

A.



B.

**Figure 3.32:**

Effect of hemin on H and L-Ft in J16 and HJ16 cell lines.

J16 and HJ16 cell lines were treated with 20 μ M hemin and were then collected at various times (i.e. 2, 4, 6, 8, 18, and 24 h). Whole cellular extracts were prepared for Ferritin ELISA (see section 2.10) to investigate the roles of H and L-Ft (A. and B., respectively). These results are expressed as mean \pm standard deviation (n=3).

* : $p < 0.05$ significant difference between corresponding control.

NS : Non-significant difference between corresponding control.

+ : $p < 0.05$ significantly different when compared with the other cell line.

Ferritin expression was also increased 6-fold following overnight treatment with hemin in macrophages (Mehlhase *et al*, 2005). A strong up-regulation of both H- and L-Ft chains was reported in HeLa cells after iron administration (Cairo *et al*, 1985). On the contrary, only H-Ft was induced after hemin treatment in bovine artery endothelial cells (Lin *et al*, 1998), L-Ft on the other hand was unaffected. Incubation of cells for 24 h in CM following 18 h hemin treatment, increased significantly the levels H- and L-Ft in both cell lines (see table 3.7-d figure 3.30-B1,B2).

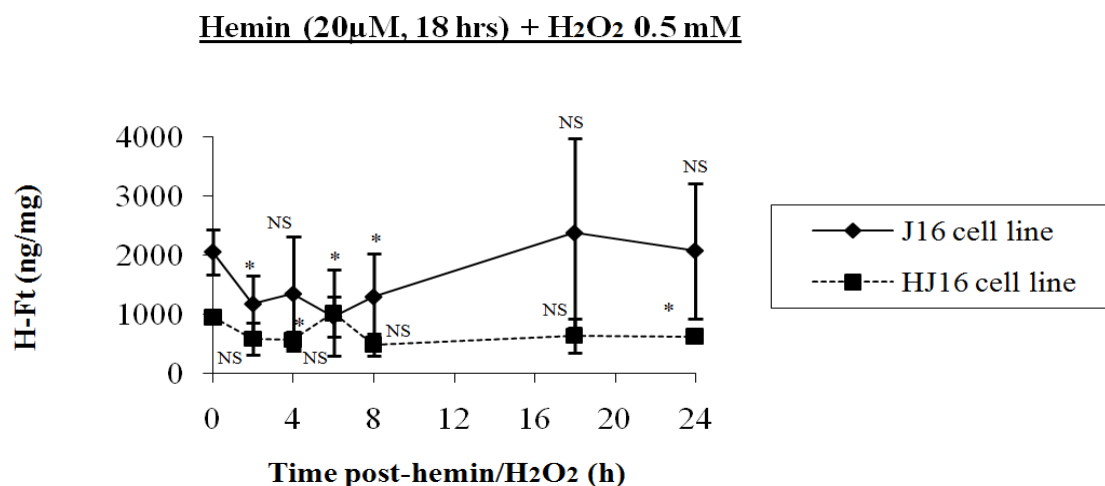
The time course experiment revealed that iron loading prior to H₂O₂ treatment decreased the H-Ft levels in J16 cells only at early hours following treatment (i.e. 2, 6, and 8 h post- H₂O₂). While in HJ16, significant decrease in H-Ft was only apparent at 4 and 24 h post-H₂O₂ treatment. The L-Ft time course study revealed that the L-Ft levels remain unchanged in HJ16 cells but it was slightly decreased in J16 cells at 4, 8, 18 and 24 h time points (see figure 3.33).

ELISA performed *immediately* after the exposure of hemin-treated cells (20µM, 18 h) to 0.5 mM H₂O₂ revealed an already significant increase in the H-Ft and L-Ft levels in J16 cell line (i.e. up to 5-fold of the control value) (see figure 3.32-A1,A2). Both H-Ft and L-Ft were also induced in HJ16 cells (i.e. up to 18-fold and 5-fold of the control values, respectively) (see figure 3.32 A1,A2). Following 24 h incubation in CM, H-Ft and L-Ft were also strongly induced in J16 cells (i.e. 6-fold and 4-fold of the control values, respectively). In HJ16 cells, H-Ft and L-Ft were also strongly induced (i.e. up to 12-fold and of the control values) (see figure 3.32 B1,B2).

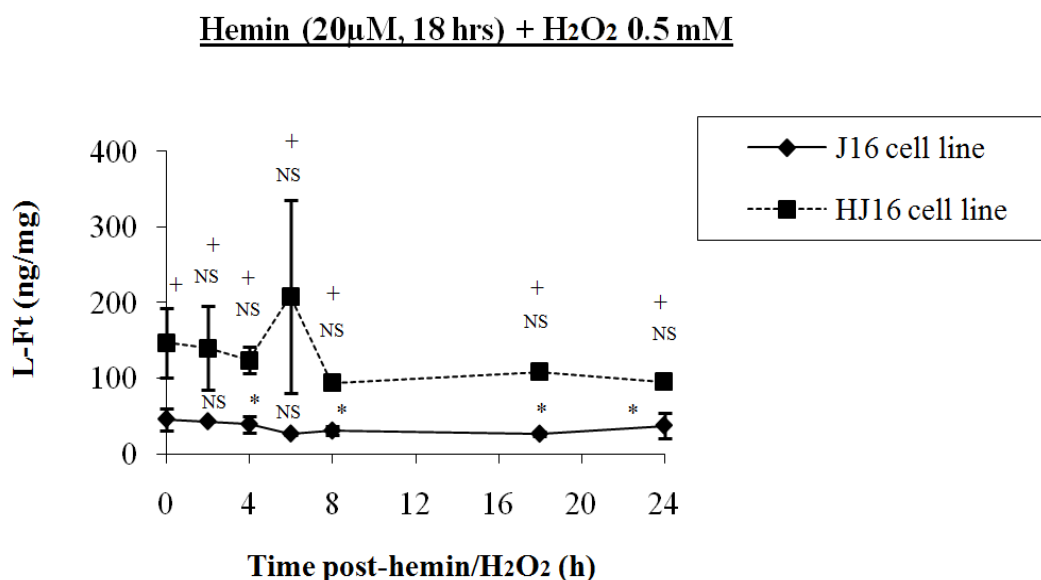
3.4.3.5 Effect of combined DFO/hemin ± H₂O₂ on the Ft levels

Finally the effect of hemin and DFO treatment with and without H₂O₂ treatment was also investigated. When the ELISA was performed *immediately* in J16 cells, 20 µM hemin (18 h) + 1mM DFO (2 h) significantly increased the H-Ft and L-Ft (i.e. up to 2-fold and 4-fold of the control value, respectively) (see figure 3.32 A1,A2). The levels of H-Ft and L-Ft were also significantly induced in HJ16 cells (i.e. up to 10-fold and 7-fold of the control value, respectively) (see figure 3.30 A1,A2). Following 24 h incubation in CM, the levels of H-Ft and L-Ft were significantly induced in J16 cells (i.e. up to 2-fold and 3-fold of the control value, respectively) (see figure 3.30-B1,B2).

A.



B.

**Figure 3.33:**

Effect of 20 μ M hemin + 0.5 mM H₂O₂ on H and L-Ft in J16 and HJ16 cell lines.

J16 and HJ16 cell lines were treated overnight with 20 μ M hemin and then with an intermediate dose of H₂O₂ (i.e. 0.5 mM). Cells were collected at various times (i.e. 2, 4, 6, 8, 18, and 24 h) and used to prepare whole cellular extracts for Ferritin ELISA (see section 2.10) to investigate the roles of H and L-Ft (A. and B., respectively). These results are expressed as mean \pm standard deviation (n=3).

* : $p < 0.05$ significant difference between corresponding control.

NS : Non-significant difference between corresponding control.

+ : $p < 0.05$ significantly different when compared with the other cell line.

This was also seen in HJ16 cells, levels of H-Ft and L-Ft were also significantly induced in HJ16 cells (i.e. up to 8-fold and 6-fold of the control value, respectively) (see figure 3.30-B1,B2).

ELISA performed *immediately* following H₂O₂ treatment of combined hemin-DFO cells, revealed a significant increase in the levels of H-Ft and L-Ft in J16 cells (i.e. up to 3-fold and 2-fold of the control value, respectively) (see figure 3.32 A1,A2). The levels of both H-Ft and L-Ft were also significantly induced in HJ16 cells (i.e. up to 14-fold and 8-fold of the control values, respectively) (see figure 3.32 A1,A2). Following 24 h incubation in CM, the levels of H-Ft and L-Ft were also significantly induced in J16 cells (i.e. up to 2-fold and 4-fold of the control values, respectively) (see figure 3.32 B1,B2). This was also seen in HJ16 cells, as levels of H-Ft and L-Ft were also significantly induced following hemin-DFO- H₂O₂ treatment (i.e. up to 8-fold of the control value) (see figure 3.32 B1,B2).

3.4.3.6 Mitochondrial ferritin in the J16 and HJ16 cell line

Mitochondrial ferritin (Mt-Ft) was also measured in both cell lines. In the J16 cell line Mt-Ft basal level was 0.53 ng/mg and 1.52 ng/mg in HJ16 cells. In J16 cell line, Mt-Ft levels following either hemin or DFO treatment prior H₂O₂ treatment or H₂O₂ treatment alone, were negligible. On the other hand, in the HJ16 cell line, Mt-Ft was increased up to 4-fold after 0.5 mM H₂O₂ treatment (measured 24 h following the treatment), overnight treatment with 20 µM hemin (measured 24 h following the treatment), and H₂O₂ treatment (0.5 mM) following overnight treatment with 20 µM hemin (measured *immediately* following the treatment). It was also increased up to 5-fold after overnight treatment with 100 µM DFO (measured 24 h following the treatment). Mitochondrial ferritin (Mt-Ft) is currently under investigation in our cell model.

3.4.4 The role of iron-mediated lysosomal damage in J16 and HJ16 cells

Since lysosomal iron release and necrosis have been related (see section 1.5.1) we wanted to a great extent understand this relationship in our cell model. To investigate the role of iron-mediated lysosomal damage in both acute and chronic oxidative stress conditions, the lysosomal damage was monitored by three

independent assays: (1) Neutral red uptake assay (2) Lysosensor immunofluorescence, and (3) Cathepsin B immunocytochemistry.

3.4.4.1 Neutral red uptake assay

Primarily, the effect of H₂O₂ treatment on lysosomal damage in both J16 and HJ16 cell lines was investigated via Neutral red (NR) uptake assay. Figure 3.34 clearly demonstrates that the lysosomal membranes in the parental J16 cells are very sensitive to H₂O₂ treatment. However, in the HJ16, cells the lysosomal membrane were very resistant to the same treatment.

Using the same approach, in J16 cells, we found that both DFO and hemin protected the cells from lysosomal damage (see figure 3.35). This is in agreement with our previous results showing that these two compounds protected J16 cells from H₂O₂-induced necrosis. In HJ16 cells (see figure 3.36), the scenario was quite different: Interestingly DFO pre-treatment (unlike the necrosis data, see figure 3.15) had no significant protective effect when compared with cells treated with H₂O₂ alone. Hemin, on the other hand, promoted more lysosomal damage in HJ16.

The lysosomal damage was also investigated in both cell lines after combined hemin (i.e. 20 µM for 18 h) - DFO (i.e. 1mM for 2 h) treatment. It was shown that DFO treatment following iron loading for 18 h (see figure 3.37) protected both cell lines from lysosomal damage. These results are in agreement with necrosis data using Flow cytometry (see section 3.4.2).

3.4.4.2 Lysosensor immunofluorescence

The LysoSensorTM Green DND-153 was used to monitor the integrity of lysosomal membranes after relevant treatments. As can be seen in figure 3.38, H₂O₂ damages the lysosomes in J16 cells in a dose-dependent manner (i.e. 0.1, 0.5, and 1mM) as observed by the loss of fluorescence due to the leakage of the dye to the cytosol. However, overnight treatment of J16 cells with either DFO or hemin protected the lysosomes against H₂O₂-induced damage. This is in agreement with the NR assay and the necrosis data using Flow cytometry. In contrast to J16 cells, the lysosomes in HJ16 cells were quite resistant to H₂O₂ treatment (see figure 3.39). Indeed, intact lysosomes could be detected even when cells were exposed to a high dose of H₂O₂ (i.e. 1mM).

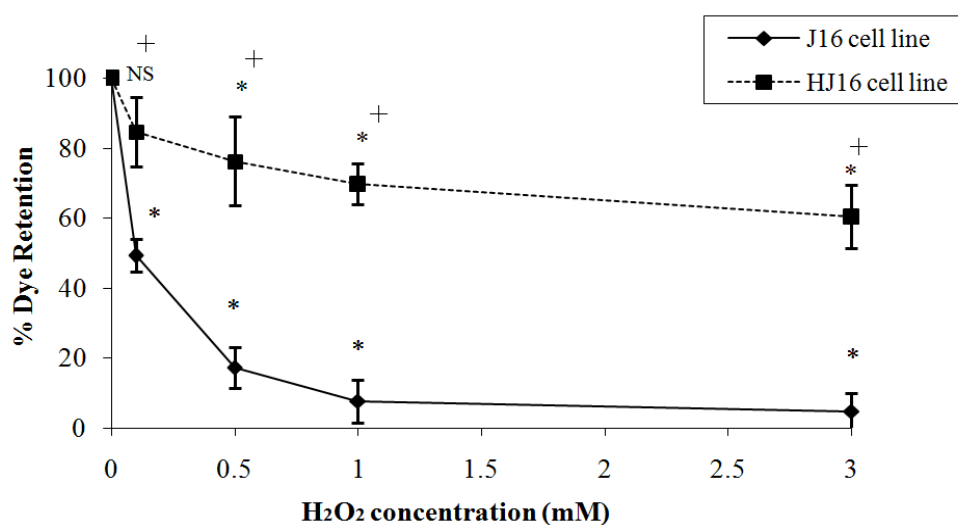


Figure 3.34 :

Effect of different concentrations of H₂O₂ treatment on J16 (parental) and HJ16 (H₂O₂-resistant) cell lines (Analysis : NR assay).

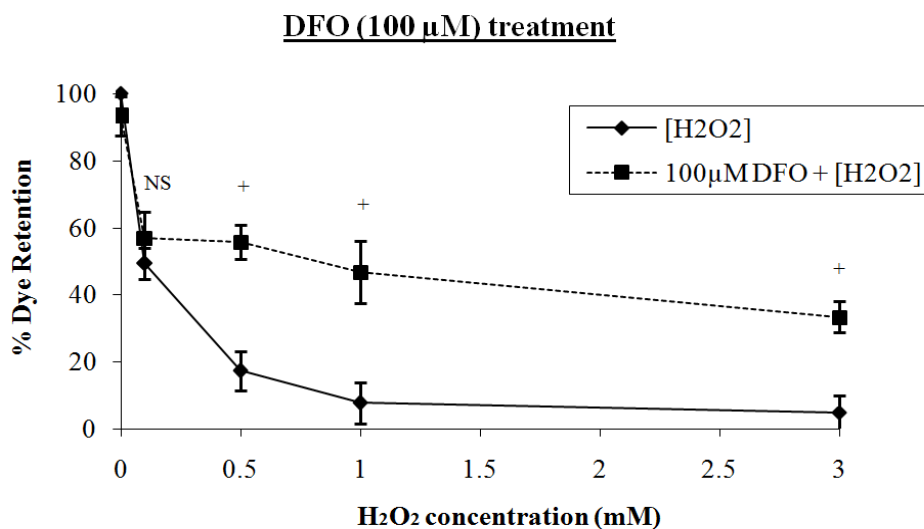
Neutral red assay was performed 24 h following H₂O₂ treatment (see section 2.11). These results are expressed as mean \pm standard deviation (n=3)

* : $p < 0.05$ significant difference between corresponding control.

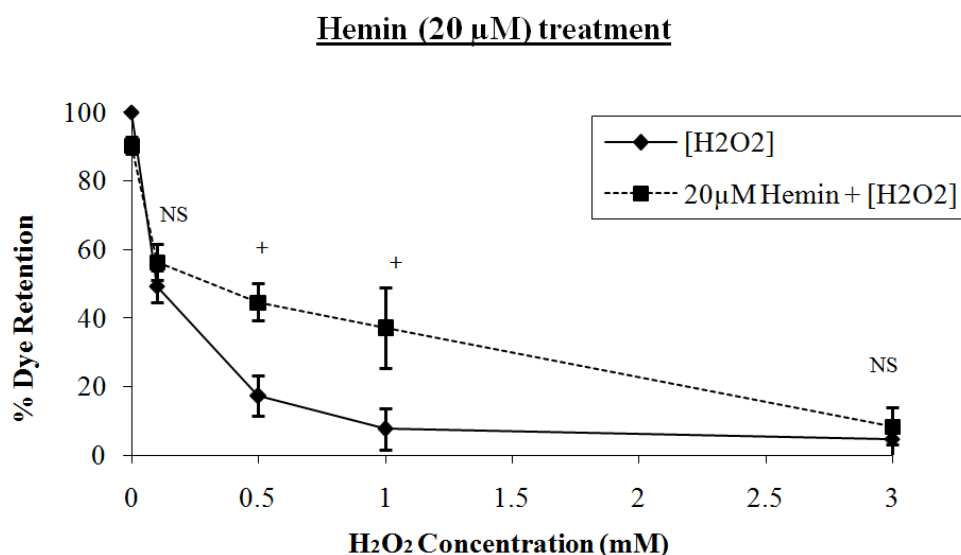
NS : Non-significant difference between corresponding control.

+ : $p < 0.05$ significantly different when compared with the corresponding J16 cells.

A.



B.

**Figure 3.35 :**

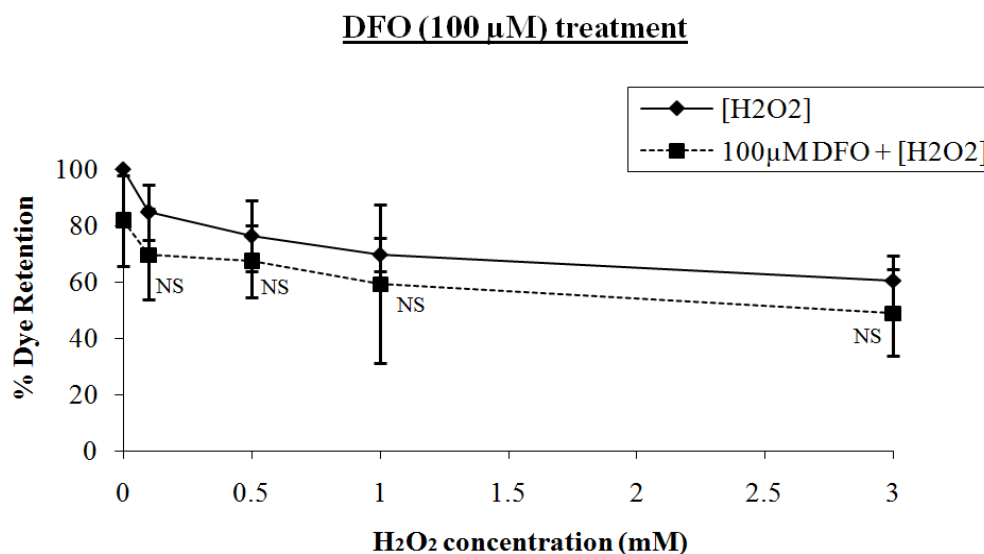
The assessment of iron chelation and loading on lysosomal damage in J16 cell line (parental cells) - (Analysis : NR assay).

J16 cells were pretreated with either 100 μ M DFO (A) or 20 μ M hemin (B) for 18 h before H₂O₂ treatment. Neutral red (NR) assay was performed 24 h following H₂O₂ treatment (see section 2.11). These results are expressed as mean \pm standard deviation (n=3).

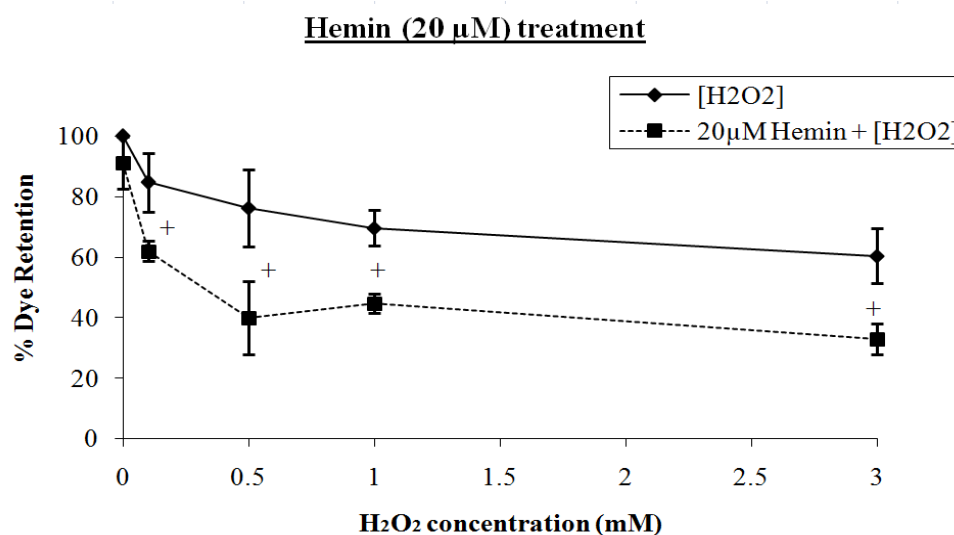
+ : $p < 0.05$ significant difference between DFO (A) or hemin (B) pre-treated cells and cells treated with H₂O₂ alone.

NS : Non-significant difference between DFO (A) or hemin (B) pre-treated cells and cells treated with H₂O₂ alone.

A.



B.

**Figure 3.36 :**

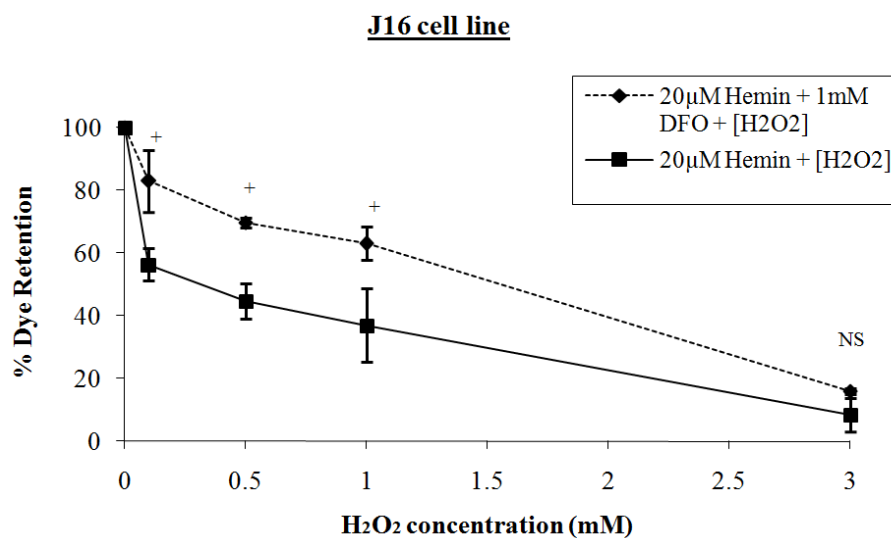
The assessment of iron chelation and loading on lysosomal damage in HJ16 cell line (H₂O₂-resistant cells) - (Analysis : NR assay).

HJ16 cells were pretreated with either 100 μ M DFO (A) or 20 μ M hemin (B) for 18 h before H₂O₂ treatment. Neutral red assay was performed 24 h following H₂O₂ treatment (see section 2.11). These results are expressed as mean \pm standard deviation (n=3).

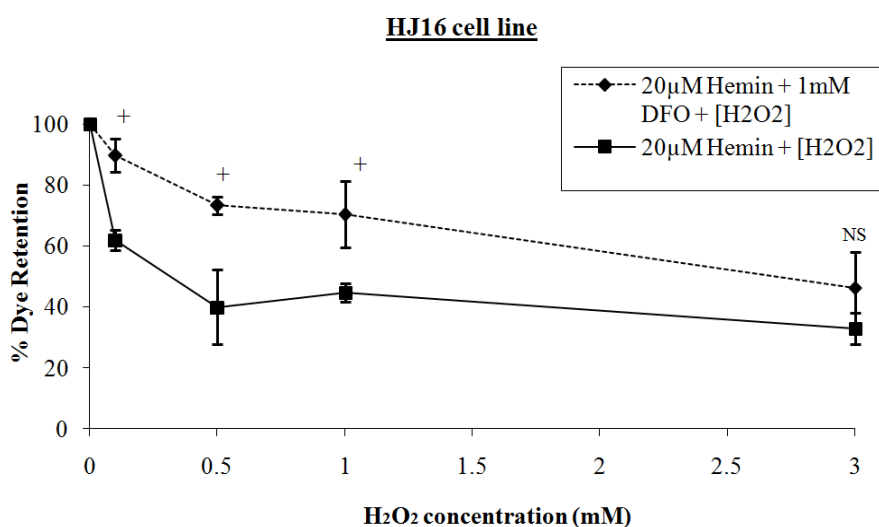
+ : $p < 0.05$ significant difference between DFO (A) or hemin (B) pre-treated cells and cells treated with H₂O₂ alone.

NS : Non-significant difference between DFO (A) or hemin (B) pre-treated cells and cells treated with H₂O₂ alone.

A.



B.

**Figure 3.37 :**

The assessment of DFO treatment following iron loading prior to H₂O₂ treatment on lysosomal damage in J16 (A) and HJ16 (B) cell lines (Analysis : NR assay).

Both cell lines were pretreated with either 20 µM Hemin for 18 h or 20 µM Hemin for 18 h and then 1mM DFO for 2 h, before H₂O₂ treatment. Neutral red assay was performed 24 h following H₂O₂ treatment (see section 2.11). These results are expressed as mean ± standard deviation (n=3).

+ : $p < 0.05$ significant difference when compared with cells pre-treated with hemin and H₂O₂ alone.

NS : Non-significant difference when compared with cells pre-treated with hemin and H₂O₂ alone.

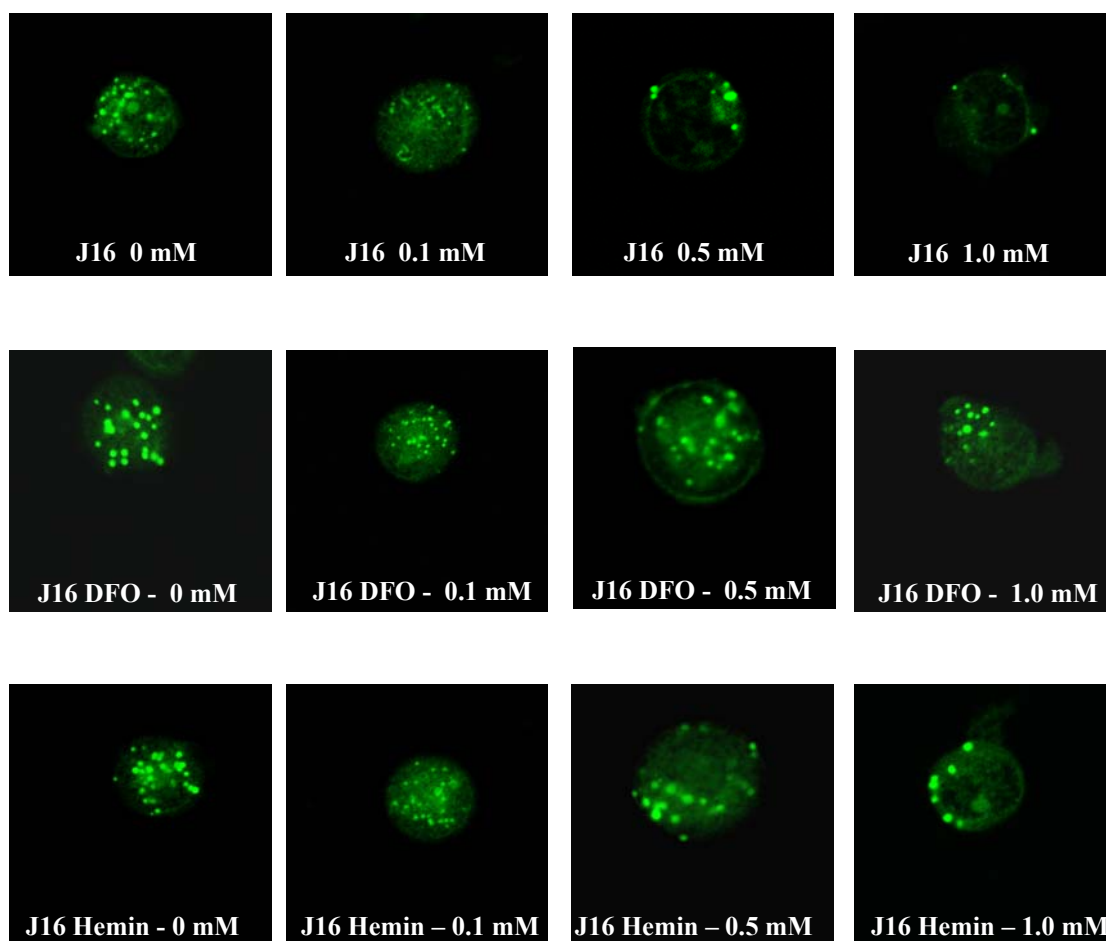


Figure 3.38 :

The effect of iron chelation and loading on the H_2O_2 -mediated lysosomal damage in J16 cell line (parental cells).

J16 cells were pre-treated with either 100 μM DFO (second row) or 20 μM hemin (third row) for 18 h before H_2O_2 treatment (i.e. 0.1, 0.5, and 1mM). The Lysosensor assay (see section 2.12) was performed 24 h following H_2O_2 treatment. The photographs are representative of three experiments.

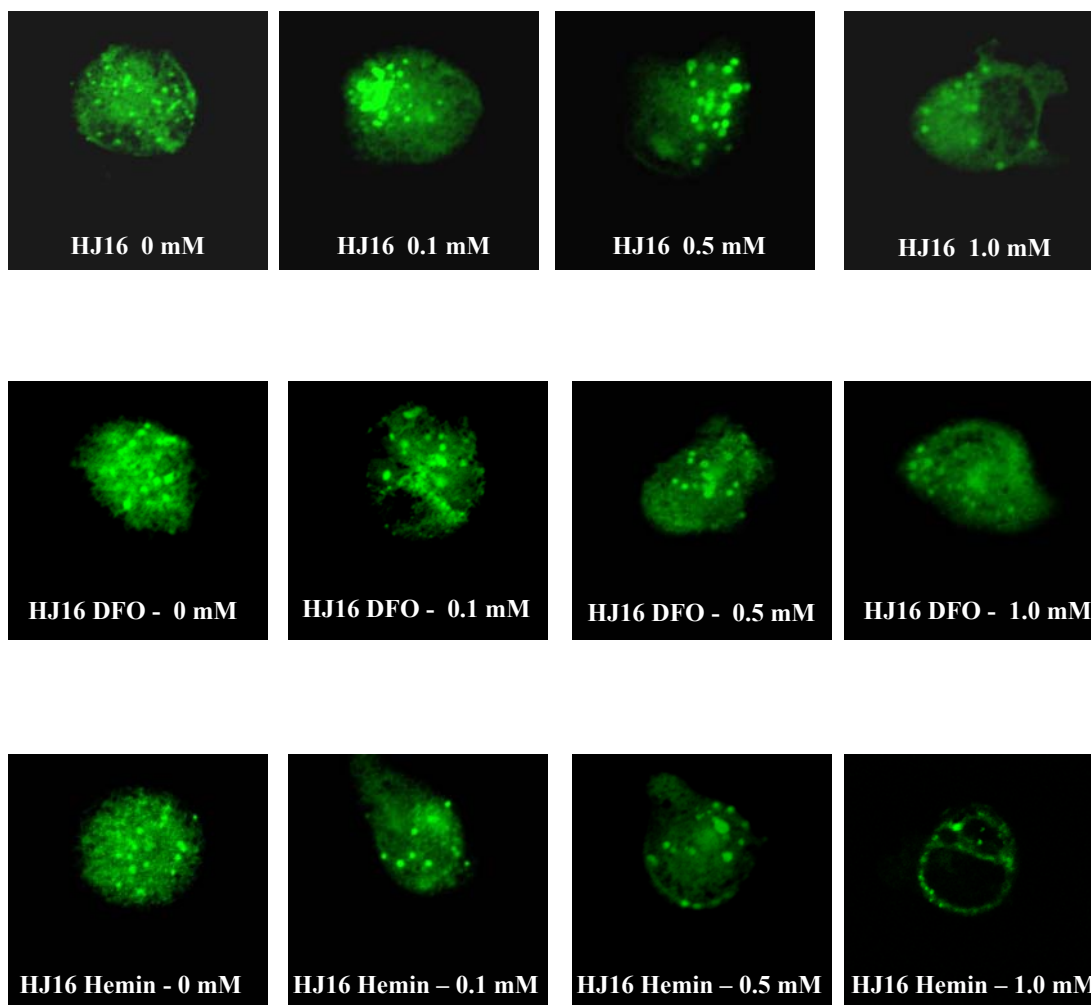


Figure 3.39 :

The effect of iron chelation and loading on the H_2O_2 -mediated lysosomal damage in HJ16 cell line (H_2O_2 -resistant cells).

HJ16 cells were pre-treated with either 100 μ M DFO (second row) or 20 μ M hemin (third row) for 18 h before H_2O_2 treatment (i.e. 0.1, 0.5, and 1mM). The Lysosensor assay (see section 2.12) was performed 24 h following H_2O_2 treatment. The photographs are representative of three experiments.

Overnight treatment of HJ16 cells with DFO had no significant effect on the lysosomal integrity. Hemin pre-treatment on the other hand caused dose-dependent damage to the lysosomes following H₂O₂ insult. The latter data are found to be in agreement with the NR assay and the necrosis data by Flow cytometry.

3.4.4.3 Cathepsin B immunocytochemistry

Cathepsin B is a cysteine protease found within the lysosomes. It has been implicated in diseases such as arthritis and cancer. When secreted, it has been shown to degrade the extracellular matrix proteins (Roshy *et al*, 2003). The results obtained from Cathepsin B immunocytochemistry confirmed the results shown with either NR or Lysosensor assays. In J16 cells (see figure 3.40), both DFO and hemin pre-treatments protected the cells against lysosomal membrane damage induced by H₂O₂, whereas in HJ16 cells (see figure 3.41), only hemin pre-treatment was shown to damage the lysosomes following H₂O₂ exposure.

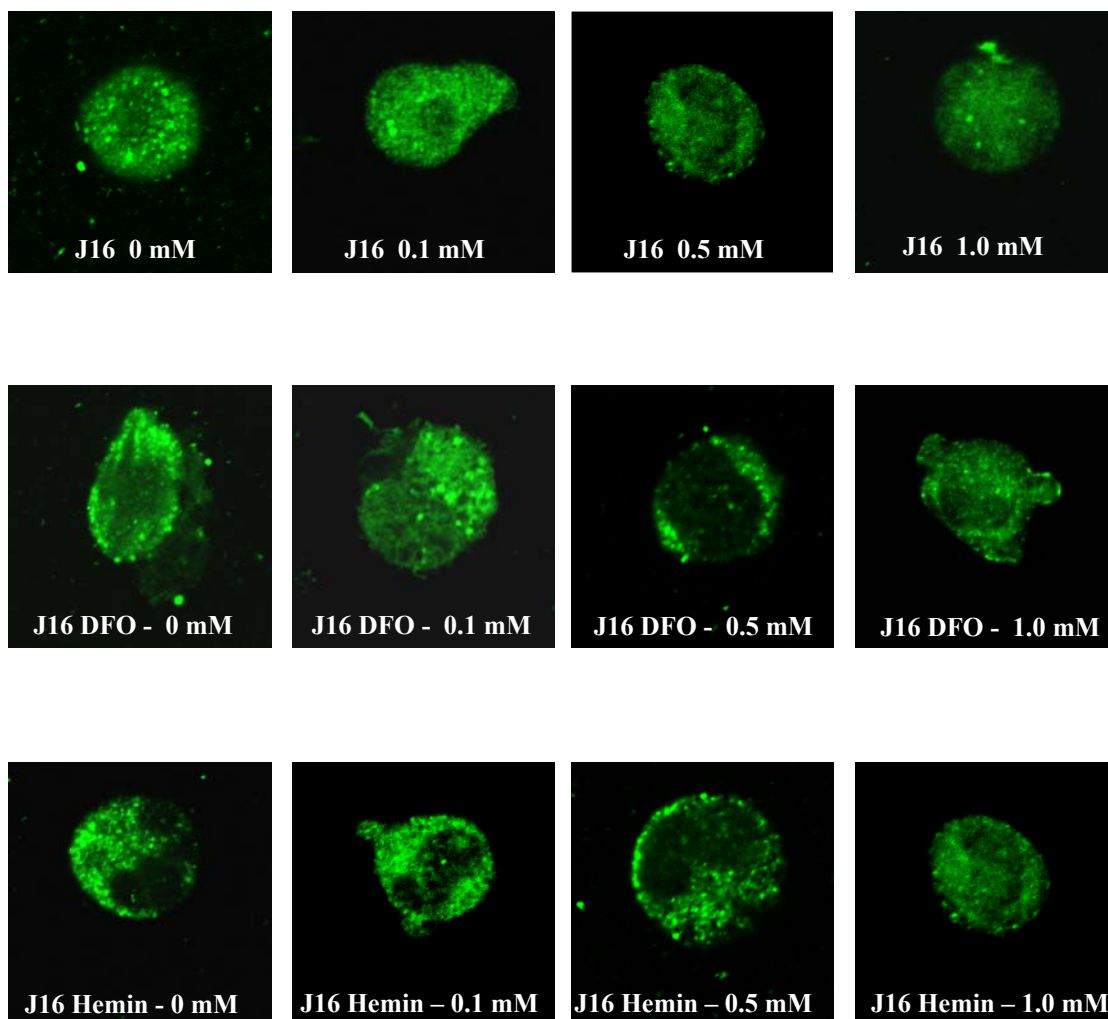


Figure 3.40:

The effect of iron chelation and loading on the H_2O_2 -mediated lysosomal damage in J16 cell line (parental cells).

J16 cells were pre-treated with either 100 μ M DFO (second row) or 20 μ M hemin (third row) for 18 h before H_2O_2 treatment (i.e. 0.1, 0.5, and 1mM). Cathepsin B immunocytochemistry (see section 2.13) was performed 24 h following H_2O_2 treatment. The photographs are representative of three experiments.

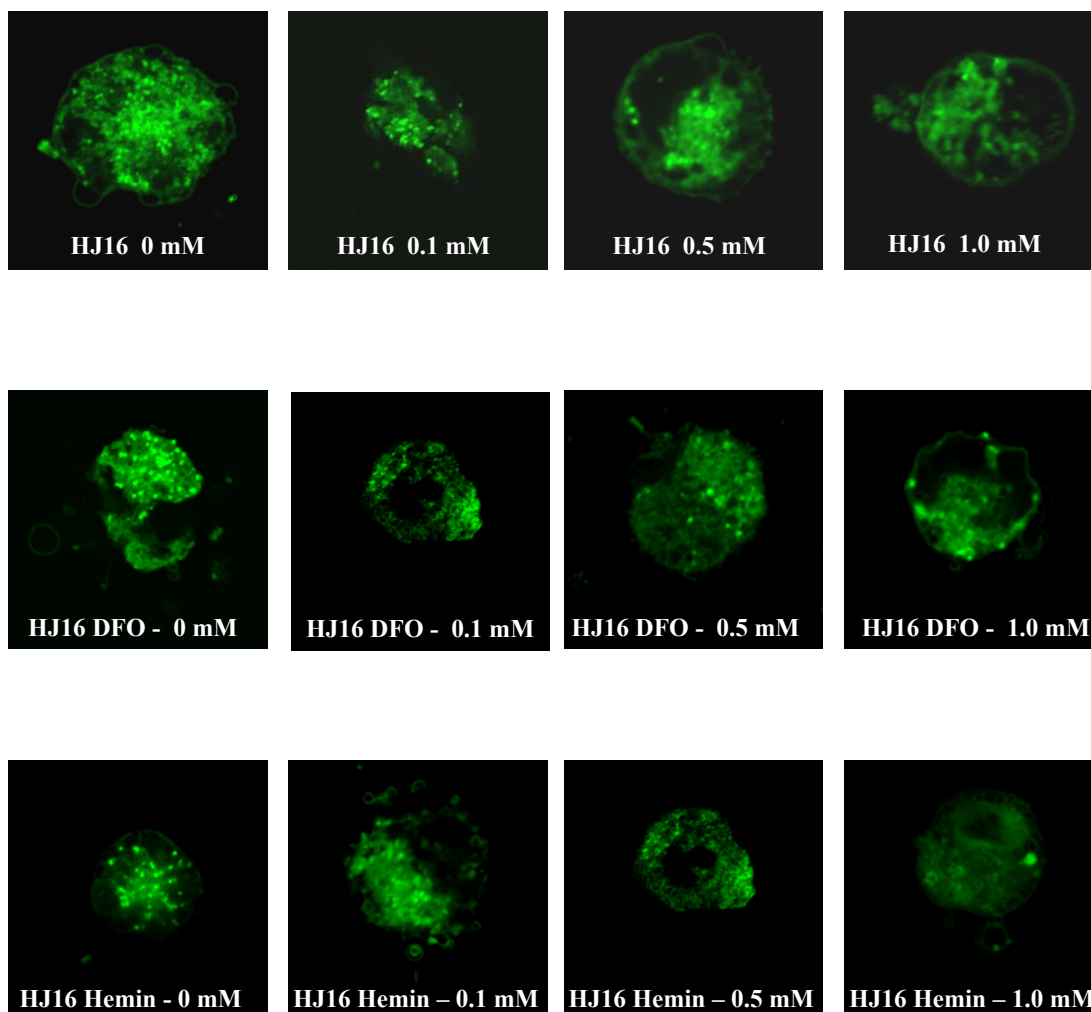


Figure 3.41 :

The effect of iron chelation and loading on the H_2O_2 -mediated lysosomal damage in HJ16 cell line (H_2O_2 -resistant cells).

HJ16 cells were pre-treated with either 100 μM DFO (second row) or 20 μM hemin (third row) for 18 h before H_2O_2 treatment (i.e. 0.1, 0.5, and 1mM). Cathepsin B immunocytochemistry (see section 2.13) was performed 24 h following H_2O_2 treatment. The photographs are representative of three experiments.

3.5 Preliminary clinical data

A preliminary study on human and rat fibroblasts was conducted in parallel with the current study (see section 2.16). In addition to this, LPI measurements of normal, RA and OA synovial fluid (SF) were performed.

3.5.1 MTT assay

Normal (HN-1) and osteoarthritic (HOA-1) human fibroblasts cells were treated with 1, 3, 5, and 7 mM H_2O_2 . Unfortunately, MTT studies on the rheumatoid arthritic (HRA-1) cells were not possible due to the difficulty in growing and maintaining these cells. The results (see figure 3.42) revealed that both HN-1 and HOA-1 cells were resistant even to high non-physiological doses of H_2O_2 . FEK4 (human fibroblasts cell line, derived from a newborn foreskin explants) and J16 cells were added as controls. The results show that the HN-1 was the most resistant cells. HOA-1 was less resistant than HN-1 and at high doses of H_2O_2 , it was even less resistant than human primary fibroblast cell line; FEK4.

Normal (VW-1) and AA (AAVW-1) rat fibroblasts were also treated with the same concentrations of H_2O_2 (i.e. 1, 3, 5, and 7 mM) and it was quite interesting to note (see figure 3.43) that AAVW-1 were very resistant to all the doses used while VW-1 was very sensitive to the same treatment. R6 (the immortalised rat embryo fibroblast cell line) and J16 cells were added as controls.

3.5.2 LIP measurements

The LIP was measured in normal (HN-1), rheumatoid arthritic (HRA-1), and osteoarthritic (HOA-1) human fibroblasts cells. The basal and H_2O_2 -induced level of LIP was investigated (see table 3.8). The basal LIP levels of HN-1, HRA-1, and HOA-1 were so low that with this assay were undetectable (i.e. below the threshold). Because of the higher susceptibility of HOA-1 to H_2O_2 -mediated damage it was hypothesised that H_2O_2 -induced levels of LIP in HOA-1 may be higher than HN-1 following treatment with an intermediate dose of H_2O_2 (i.e. 1mM).

MTT assay with 1mM of H_2O_2 showed a decrease in the percentage of intracellular dehydrogenase activity of HN-1 to 91.5 % of the control value (i.e. 100%) and to 60.8% in HOA-1 cells.

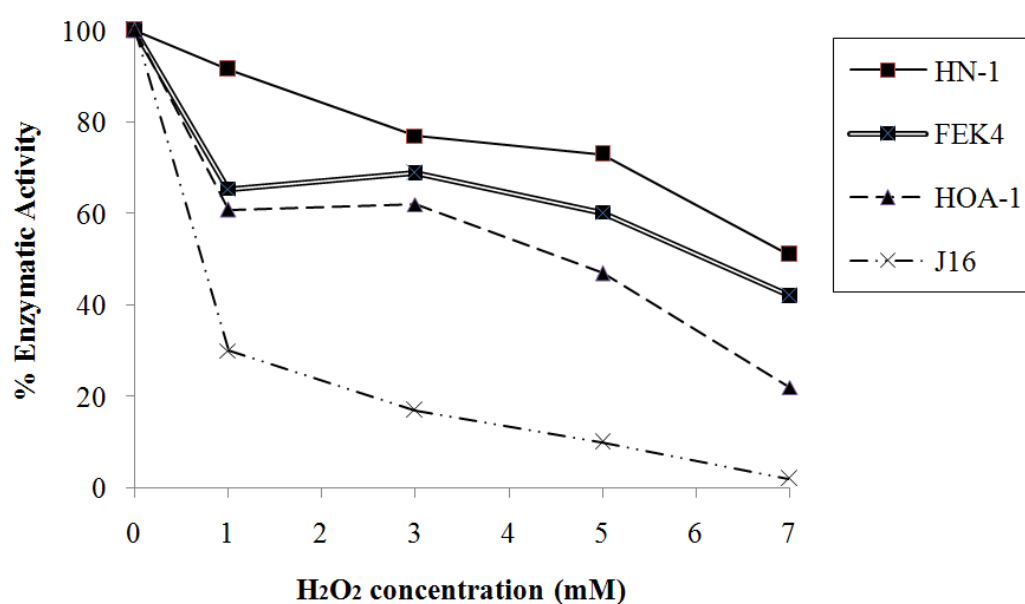


Figure 3.42 :

Effect of different concentrations of H₂O₂ on viable human cells (Analysis : MTT assay).

Normal (HN-1), osteoarthritic (HOA-1) human fibroblasts, FEK4 and J16 cells were treated with 1, 3, 5, and 7 mM H₂O₂. MTT analysis (see section 2.4) was performed 24 h following H₂O₂ treatment (n=1).

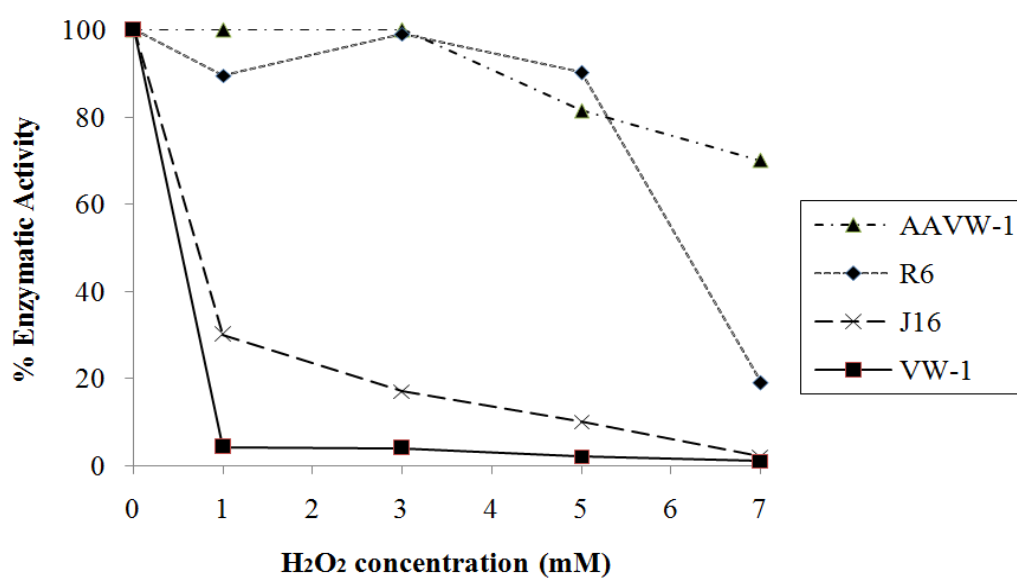


Figure 3.43 :

Effect of different concentrations of H₂O₂ on viable rat cells (Analysis : MTT assay).

Normal (VW-1) and AA (AAVW-1) rat fibroblasts, R6 (rat cell line) and J16 cells were treated with 1, 3, 5, and 7 mM H₂O₂. MTT analysis (see section 2.4) was performed 24 h following H₂O₂ treatment (n=1).

Table 3.8:

Labile iron pool (LIP) basal and H₂O₂-induced (i.e. 1mM) levels of normal (HN-1) and osteoarthritic (HOA-1) human fibroblasts.

Cells	Basal levels (μM/μg)	Post 1mM-H ₂ O ₂ (μM/μg)
HN-1	Undetectable	Undetectable
HRA-1	Undetectable	Undetectable
HOA-1	Undetectable	0.18 ± 0.06

As described in section 2.15, the LIP basal levels and H₂O₂-induced (i.e. 1mM) of both normal (HN-1) and osteoarthritic (HOA-1) human fibroblasts was measured. These results are expressed as mean ± standard deviation (n=3).

These results were in agreement with our hypothesis, since following treatment of cells with an intermediate dose of 1mM H₂O₂, the LIP levels in HOA-1 increased to a detectable level (i.e. $0.18 \pm 0.06 \mu\text{M}/\mu\text{g}$) while it remained at undetectable levels in HN-1. However, more samples are needed to validate our hypothesis. The LIP was also undetectable in HRA-1 cells.

The basal and the H₂O₂-induced (i.e. 1mM) levels of LIP were also investigated in normal (VW-1) and AA (AAVW-1) rat fibroblasts (see table 3.9). The basal levels of the LIP were undetectable in VW-1 but in AAVW-1 cells it was found to be within detectable range of $0.003 \pm 1.25 \times 10^{-5} \mu\text{M}/\mu\text{g}$. Similarly with our rat cell model, it was hypothesised that an increase in LIP will be only seen in the normal (VW-1) cells when compared to AA (AAVW-1) rat fibroblasts after H₂O₂ treatment. The rationale for this hypothesis was that at 1mM of H₂O₂, the intracellular dehydrogenase activity of VW-1 decreased to 4.2 % of the control value (i.e. 100%), and it was not modified in AAVW-1 cells. Following an intermediate dose of 1mM of H₂O₂, the LIP levels of VW-1 increased to the detectable levels and in AAVW-1 cells, the increase was interestingly more than 13-fold.

3.5.3 LPI measurements

Labile plasma iron (LPI) was also measured, as described in section 2.16 in the synovial fluid (SF) of normal, rheumatoid arthritic (RA), and oosteoarthritic (OA) patients. Synovial fluid from a normal, two RA, and six OA patients was analysed. The results (see table 3.10) show that there was no consistent pattern in these samples. The LPI of the normal patient was $0.45 \pm 0.3 \mu\text{M}$, it seems to be slightly higher in RA but it was non-significant ($p \text{ value} > 0.05$). In OA samples, some had higher value than the normal sample and others had lower values, but they were all non-significant. Clearly, more samples are needed to complement these observations.

Table 3.9:

Labile iron pool (LIP) basal and H₂O₂-induced (i.e. 1mM) of the normal (VW-1) and AA (AAVW-1) rat fibroblasts.

Cells	Basal levels (μM/μg)	Post 1mM-H ₂ O ₂ (μM/μg)
VW-1	Undetectable	0.02 ± 0.008
AAVW-1	0.003 ± 1.25 x 10 ⁻⁵	0.04 ± 0.007 * ⁺

As described in section 2.15, the LIP basal levels and H₂O₂-induced (i.e. 1mM) of both of the normal (VW-1) and AA (AAVW-1) rat fibroblasts was measured. These results are expressed as mean ± standard deviation (n=3).

* : p < 0.05 significantly different when compared with the basal levels.

+ : p < 0.05 significantly different when compared with the corresponding VW-1.

Table 3.10 :

Labile plasma iron (LPI) measurements of synovial fluid from normal, rheumatoid arthritic (RA), and osteoarthritic (OA) patients.

Condition	LPI (μM)
Normal knee	0.45 ± 0.3
RA knee	0.47 ± 0.09 ^{NS}
RA knee	0.54 ± 0.71 ^{NS}
OA knee	1.4 ± 1.06 ^{NS}
OA knee	0.29 ± 0.19 ^{NS}
OA knee	0.76 ± 0.36 ^{NS}
OA knee	0.44 ± 0.2 ^{NS}
OA knee	0.47 ± 0.29 ^{NS}
OA knee	0.04 ± 0.01 ^{NS}

LPI was measured as described in section 2.16. These results are expressed as mean \pm standard deviation (n=3).

NS : non significantly different from the normal sample.

CHAPTER FOUR

DISCUSSION

Inflammation is a term used to illustrate the body's complex physiological response, whether acute or chronic, to tissue injury (Underwood, 1996). The role of the acute response is to clear dead cells from the site of the injury, to protect the site against any pathogens, and to permit the immune system to gain access to the site of inflammation (Junqueira *et al*, 1986). It is crucial that inflammatory reactions are self-limited upon e.g. elimination of the triggering factors, if not, they do perpetuate to chronic inflammation (Schett, 2008). The transition between the acute phase and the chronic phase is largely dependent on the persistence of the inflammatory cause. When the cause persists, chronic inflammation follows, which may last for a prolonged duration of time - weeks, months, or even indefinitely, and subsequently the cell population changes (Feghali and Wright, 1997). Lymphocytes and macrophages are the predominant cells in chronic inflammation (Junqueira *et al*, 1986; Underwood, 1996; Stevens and Lowe, 1999). In the inflamed area, these cells engulf the remains of cells and fibres and participate in the production of antibodies against invading microorganisms (Junqueira *et al*, 1986). Lymphocytes are also the key components in the onset and exacerbation of autoimmune diseases and the cytokines produced by them have a great impact on disease progression (Horwood, 2008). Cytokines are the key mediators of inflammation and can be found in abundance in the joints and the blood of patients suffering from rheumatoid arthritis (Christodoulou and Choy, 2006).

Rheumatoid arthritis (RA) is an example of a chronic auto-immune inflammation disease. It primarily affects the joints and ultimately leads to their destruction (Huber *et al*, 2006). Several studies indicate that during an inflammatory response, considerable amounts of ROS are generated that participate in the aetiology and/or the progression of the condition. For example in an inflammatory environment, lymphocytes are exposed to extensive quantities of H₂O₂ produced by macrophages and neutrophils as a result of the inflammatory response. Therefore, oxidative stress has been implicated in several physiological and pathological conditions (Vendemiale

et al, 1999), notably RA. Superoxide anion and H_2O_2 *per se* are not injurious but may become so in the presence of redox active iron or other transition metals. The potentially harmful free ‘labile’ iron is recognised as an important promoter of oxidative stress through aiding the production of ROS and thus a potential mediator of the inflammatory process in RA.

In addition to UVA (Morliere *et al*, 1997 and Pourzand *et al*, 1999) and visible light irradiation (Ohishi *et al*, 2005), it has already been shown that the exposure of cells to H_2O_2 (see section 1.3.6) provokes an increase in the LIP that correlates with cell damage and necrotic cell death, although the mechanisms involved had not been fully understood. The lysosomal compartment seems to contain the major important cellular pool of labile iron (Petrat *et al*, 2001; Kakhlon and Cabantchik, 2002; Persson *et al*, 2003) since the degradation of many macromolecules that are rich in iron (e.g. ferritin and mitochondrial electron-transport complexes) occurs in the lysosomes (Radisky and Kaplan, 1998 and Kurz *et al*, 2007) making these organelles vulnerable to oxidative stress (Persson *et al*, 2005). Therefore, understanding the link between lysosomal membrane damage and the iron may define pathological mechanisms associated with oxidative stress and lysosomal activity.

In this present study, we have used H_2O_2 as an oxidising agent, since treatment with this agent is commonly used to study the effect of ROS in biochemical pathways and it diffuses easily across cellular compartments (Auntes and Cadenas, 2000). It is known that H_2O_2 is generated during normal metabolism and produced in large quantities by phagocytic cells at inflammatory sites (Hylop *et al*, 1995). Several studies have shown the crucial role iron in inflammatory diseases such as RA; but none, to our knowledge, had differentiated between the role of iron in both acute and chronic phases in the disease and the origin of this ‘free’ iron. Therefore our primary aim was to investigate the role of iron in both acute and chronic oxidative conditions.

To achieve our aim we have extensively studied two cell lines which were Jurkat cells, human T-cell leukaemia cell line. Our model consisted of two human Jurkat T cell lines of “parental (J16)” and “ H_2O_2 adapted/resistant/stressed (HJ16)” types. J16 cells were used to mimic the acute phase of oxidative stress. The HJ16 cell line was used to mimic the chronic phase since unpublished data from N.D Hall’s laboratory

(Department of Pharmacy and Pharmacology, University of Bath) have shown that HJ16 cells have characteristics similar to that of rheumatoid synovial T cells.

A. Yiakouvaki from this laboratory (PhD Thesis, 2003 – University of Bath) has already characterised these Jurkat T cell lines in terms of antioxidant defence and modulation of intracellular LIP following H_2O_2 . Overall her results provided a link between the amount of H_2O_2 -induced labile iron release and the extent of oxidative damage and cell death in Jurkat T cells. Furthermore the study showed that adaptation of Jurkat T cells to H_2O_2 can influence the basal level of antioxidant enzymes that is likely to contribute to resistance of HJ16 cells to H_2O_2 insult.

This thesis has continued the study of Yiakouvaki (2003) by further characterising the differential response of parental J16 and H_2O_2 -resistant HJ16 Jurkat T cells to H_2O_2 .

The level of resistance of Jurkat T cell lines to H_2O_2 -mediated toxicity

Tissues, in different pathological conditions, are confronted with elevated H_2O_2 concentrations derived either extra- or intra-cellularly. Overall the treatment of both cell lines with various concentrations of H_2O_2 revealed that exposure of parental J16 cells to moderate concentrations of H_2O_2 was capable of damaging half of the J16 cell line population since the percentage of live cells was found to be decreased to around 50 % of the control values. On the other hand, the HJ16 cell line showed higher resistance to H_2O_2 -mediated oxidative insult, even at doses as high as 3 mM. Flow cytometry analysis further revealed that both cell lines are highly resistant to H_2O_2 -mediated apoptotic cell death and that necrosis rather than apoptosis is responsible for H_2O_2 -induced cell death.

The ultimate response of cells to oxidative stress is cell death in the form of apoptosis or necrosis. While apoptosis is recognised as a physiological programmed process to eliminate aged, superfluous or superficially damaged cells, necrosis is usually the ultimate response of cells to severe physical- or chemical-induced acute injury. Our results show that J16 parental cells are very sensitive to acute H_2O_2 insult since they die preferentially via necrosis. The gradual adaptation of HJ16 cells to H_2O_2 on the other hand appears to have increased their tolerance to H_2O_2 -induced oxidative damage since the percentage of HJ16 cells dying by necrosis is dramatically lower than in parental J16 cells. The higher resistance of HJ16 cells to H_2O_2 -induced

necrotic cell death is likely to be related to higher detoxification of H_2O_2 by intracellular antioxidant molecules/enzymes such as catalase, GPx and glutathione. The comparative study carried out by A. Yiakouvaki has already indicated that HJ16 cells have higher intracellular glutathione content and GPx activity when compared to J16 cells. However catalase activity was quite similar between the two cell lines. The study concluded that catalase should have a minor role in detoxifying H_2O_2 as it is located in peroxisomes and its access to cytosolic H_2O_2 is limited. However both GPx and glutathione that is required to complete the catalytic cycle of H_2O_2 are reside in the cytosol.

Interestingly, studies with synovial fluid have shown that RA patients have significantly higher GPx and catalase than normal controls (Biemond *et al*, 1984). GPx was also increased in the serum of patients with RA compared with the healthy control groups (Butkiene *et al*, 2007). It was therefore suggested that oxidative stress occurs in RA because of disturbance of enzymatic and non-enzymatic antioxidants systems.

In the present study it was decided to further characterise the Jurkat T cell lines cells in terms of their antioxidant defence mechanism by comparing the level of glutathione, Ft, HO-1 and HO-2 in presence or absence of H_2O_2 between parental and H_2O_2 -resistant cells.

The role of intracellular glutathione

The intracellular glutathione system within the cells acts as a homeostatic redox buffer providing a major constitutive defence against oxidants (Applegate *et al*, 1992). To determine whether the total intracellular levels of glutathione play a role in increased resistance of HJ16 cell line to H_2O_2 , the basal glutathione level was monitored in both parental (J16) and H_2O_2 -resistant (HJ16) cell lines. Furthermore an attempt was made to deplete the intracellular level of glutathione in both cell lines (i.e. by BSO) to demonstrate the possible link between the intracellular level of glutathione and susceptibility of both cell lines to H_2O_2 -mediated cytotoxicity.

The results revealed that in agreement with Yiakouvaki's data, HJ16 cells possess significantly higher (i.e. 3.4-fold) 'basal' levels of intracellular glutathione than J16 cells. However it was important to investigate the fate of glutathione following H_2O_2 treatment in our Jurkat cell models and to check whether the possible

modulation of glutathione levels by H_2O_2 insult could influence the susceptibility of Jurkat cells to necrotic cell death.

Glutathione is believed to be a very important cellular antioxidant compound, as its depletion is used to induce oxidative stress (Recalcati *et al*, 2003 and Tacchini *et al*, 2006). In fact, several studies have shown that the depletion of intracellular glutathione sensitises cell populations to several circumstances e.g. aerobic ionising radiation and cytotoxic drugs. For example glutathione depletion (by BSO) sensitises cultured human lymphoid cells to γ radiation (Dethmers and Meister, 1981), therefore it is regarded as a major protective agent against such radiation. Glutathione not only protects cells from the cytotoxic UVA damage, but also against the damage cause by UVB radiation (Tyrrell and Pidoux, 1988). It was also shown that yeast cells developed an increased sensitivity against H_2O_2 and ionising radiation following the depletion of glutathione (Sipos *et al*, 2002). In the present study we also demonstrated that the susceptibility of both cell lines to H_2O_2 -mediated cytotoxicity was substantially increased following the depletion of the intracellular glutathione level. These results are in agreement with the previous observations made by others indicating that intracellular glutathione provides a constitutive mechanism of defence against ROS during oxidative stress conditions.

Oxidative stress in the form of UVA radiation (320 - 380 nm) and H_2O_2 have been shown to deplete intracellular glutathione (Lautier *et al*, 1992; Brunk *et al*, 1995^a; Hempel *et al*, 1996). Therefore, the levels of total intracellular glutathione were measured following H_2O_2 treatment in J16 and HJ16 cell lines. Our results showed that H_2O_2 doses higher than 0.1 mM depleted significantly the total intracellular glutathione content in J16 cell line. However in HJ16 cells, H_2O_2 treatment only decreased to half the total intracellular level of glutathione. These results strongly suggest that chronic exposure of HJ16 cells to H_2O_2 provokes an adaptive mechanism preventing the total depletion of total intracellular glutathione in these cells. The latter should almost certainly contribute to the resistance of HJ16 cells to the high doses of H_2O_2 .

Characterisation of the response of NF- κ B to H_2O_2 treatment

The NF- κ B complex has been shown to be activated in response to multiple stimuli many of which are possibly mediated by the generation of ROS (Piette *et al*, 1997 and Gilston *et al*, 2001). In response to these stimuli, NF- κ B complex

activation has been examined in neutrophils, macrophages, and lymphocytes (reviewed in Makarov, 2001). The inducibility of the NF- κ B complex in response to H₂O₂ is cell-specific. Furthermore it is not clear whether this response will be lost if cells are chronically adapted to H₂O₂ treatment, in the case of HJ16 cell line. Therefore the inducibility of NF- κ B complex, by Electrophoretic Mobility Shift Assay (EMSA) and immunocytochemistry was investigated in both J16 and HJ16 cell lines following H₂O₂ treatment. Our results demonstrated that NF- κ B complex is present and induced by H₂O₂ in both J16 and HJ16 cells, although the induction was higher in HJ16 cells. These findings are in conflict with other studies that have shown that the induction of NF- κ B is strongly suppressed in cells pre-exposed to sources of oxidative stress such as H₂O₂ (Lahdenpohja *et al*, 1998).

The NF- κ B complex has been shown to be activated in cancer cells and also after chemotherapy or radiotherapy, and therefore it has been associated with the resistance of these cells to apoptosis (reviewed in Piva *et al*, 2006 and Sethi *et al*, 2008). The NF- κ B complex therefore plays an important role in cell survival (Habens *et al*, 2005). The higher activation of NF- κ B by H₂O₂ in HJ16 cells could be seen as another adaptive mechanism in these cells increasing their survival against H₂O₂-induced oxidative damage and necrotic cell death. To this regard, several recent studies have provided evidence about the existence of a prosurvival pathway initiated by NF- κ B that appeared to be responsible for the radioadaptive response (i.e. radioresistance) in all cells (reviewed in Ahmed and Li, 2008). Furthermore it has been speculated that the inducibility of the NF- κ B complex in synovial T cells of rheumatoid arthritic patients should be low as these cells are chronically exposed to ROS. *In vitro* studies have proven that this speculation is incorrect (see section 1.6.6).

Studies by Marok *et al* (1996) and Gilston *et al* (1997) have demonstrated that NF- κ B complex is highly activated in patients with chronic inflammatory conditions such as rheumatoid arthritis. Our data appears to be in agreement with such studies. As mentioned in section 1.6.3, activation of NF- κ B can be divided into two pathways, the ‘classical’ and the ‘alternative’ pathway. The classical pathway has been proposed to be responsible for the NF- κ B activation in the RA synovium (reviewed Simmonds and Foxwell, 2008). Clearly further studies are necessary to unravel the role of NF- κ B in both oxidative stress and inflammatory conditions.

Similarly, in our cell models, further investigations are necessary to understand the mechanism underlying the higher NF- κ B activation in HJ16 cells.

The role of LIP in differential sensitivity of the J16 and HJ16 cells to H₂O₂ treatment

Hydrogen peroxide-sensitive (and ionising radiation-resistant) mouse lymphoma cell line has 3-fold higher ‘basal’ LIP levels than H₂O₂-resistant (and ionising radiation-sensitive) cells (Lipinski *et al*, 2000). However what these authors called ‘LIP’ levels in their measurements with CA-assay reflects only the CA-bound iron that is usually referred to as chelatable iron pool. The LIP according to Cabantchik and co-workers who developed the CA-assay is operationally defined as the sum of the intracellular level of CA-bound iron (i.e. [CA-Fe]) and free iron (i.e. [Fe] unbound to CA) and requires the determination of the cell-dependent dissociation constant (K_d) for CA-Fe by taking into account the cell volume. These determinations were lacking in the study by Lipinski *et al*, (2000). In our cell volume study we have observed that the HJ16 cells are significantly larger cells than the parental cells (i.e. 3.4-fold bigger than J16), therefore in all our iron studies, it was necessary to first determine the cell-dependent K_d of CA-bound iron in order to calculate the absolute level of LIP. The results demonstrated that the ‘basal’ LIP levels of both cell lines were quite similar; J16 cells (3.08 μ M \pm 0.59) and HJ16 cells (3.34 μ M \pm 0.87). However following H₂O₂ treatment, the LIP was increased by more than 3.2-fold in J16 cells (9.86 μ M \pm 0.35) and this was correlated with high necrosis. In HJ16 cells, H₂O₂ produced only a moderate increase in the basal LIP level (5.27 μ M \pm 1.12) when compared with J16 cells and this correlated to lower necrosis than in J16 cells. The lower increase of LIP in HJ16 cells after H₂O₂ treatment is likely to be part of the adaptive mechanism developed in these cells making these cells less susceptible to H₂O₂-induced oxidative iron-damage and necrotic cell death. Interestingly human epidermal keratinocytes that are naturally resistant to UVA-induced damage also show lower LIP levels than the UVA-sensitive dermal fibroblasts following UVA irradiation. The lower UVA-induced LIP levels in keratinocytes has been correlated with their low propensity to UVA-induced necrotic cell death (Zhong *et al*, 2004). It appears that in our cell model, the modulation of the

LIP levels following H_2O_2 treatment also correlates with the extent of cell damage and necrotic cell death.

To ascertain the importance of H_2O_2 -induced labile iron release in modulating the susceptibility of cells to H_2O_2 -induced necrotic cell death, both J16 and HJ16 were treated with DFO, a strong iron chelator or hemin (i.e. ferric haem) as a source of iron for 18 h prior to H_2O_2 treatment and then the level of LIP was measured following H_2O_2 treatment using the CA assay. The results demonstrated that DFO treatment abolishes both the ‘basal’ and ‘ H_2O_2 -induced’ LIP levels and necrotic cell death in both cell lines, consistent with the notion that iron chelation by DFO protects the cells against H_2O_2 -induced necrotic cell death. In the case of hemin treatment, hemin alone (i.e. when not followed by H_2O_2 treatment) did not modulate the level of LIP in J16 cells but upon H_2O_2 treatment it caused a low increase in LIP that correlated with low necrosis. This is in agreement with previous studies by Balla and co-workers showing that the endothelium’s susceptibility to H_2O_2 -mediated insults decreases following exposure to hemin or haemoglobin (Balla *et al*, 1992 and 1993). It was also demonstrated that extracellular Fe^{2+} and H_2O_2 preserved intracellular glutathione, prostaglandin H synthase, mitochondrial electron transport, and cell calcium entry, and therefore protected endothelial cells from cellular damage (Hempel *et al*, 1996). On the other hand, in HJ16 cell line, hemin treatment modulated both the ‘basal’ and ‘ H_2O_2 -induced’ LIP levels in HJ16 cells. The higher levels of LIP accumulation after overnight hemin treatment of HJ16 cells abolished their resistance to H_2O_2 -induced damage since the level of necrosis was significantly increased upon hemin- H_2O_2 treatment. These results strongly suggested that the presence of higher LIP in HJ16 cells following hemin treatment should be responsible for abolishing the resistance of HJ16 cells to H_2O_2 -mediated oxidative insult. Hydrogen peroxide can react with Fe^{3+} to form $\text{O}_2^{\cdot-}$ and if H_2O_2 is in excess, the Fe^{2+} which is formed can subsequently generate ROS via the Fenton reaction (Henle and Linn, 1997). The iron-mediated damage is very powerful and should almost certainly contribute to severe oxidative damage in HJ16 cells leading to necrotic cell death. Further investigation with time course analysis revealed that in J16 cells, hemin only caused a transient and moderate increase in the LIP levels within the first 2-4 h after treatment, but in HJ16 hemin provoked a higher accumulation of LIP levels that was sustained at least for 18 h. In HJ16 cells, the hemin-mediated increase in LIP was also concentration-dependent. The high accumulation of LIP in HJ16 cells following

hemin treatment increased dramatically the percentage of necrotic cell death, consistent with the notion that the intracellular level of LIP plays an important role in determining the level of sensitivity of these cells to H₂O₂-mediated necrotic cell death.

To further demonstrate the strict dependence of H₂O₂-induced necrotic cell death on LIP level present in the cells, hemin treatment for 18 h was followed by an additional treatment with 1 mM DFO for 2h. The latter treatment was expected to lower the hemin-mediated increase in LIP, leading to decreased necrosis by H₂O₂. The results showed that, in agreement with our hypothesis, in both cell lines DFO treatment of cells pre-treated with hemin, significantly decreases the levels of H₂O₂-induced necrotic cell death when compared to cells treated with hemin alone.

Taken together, from the above results; a picture emerged suggesting that LIP levels must be a key component in determining the extent of the sensitivity of these cells to H₂O₂-induced necrotic cell death. However it was surprising to see how the same treatment provoked two entirely different responses in the cell lines. The hemin treatment increased the resistance of J16 to H₂O₂-induced necrotic cell death but abolished the resistance of HJ16 cells. The hemin overnight treatment increased the levels of LIP in HJ16 cells but not in J16 cells. We hypothesised that the high accumulation of labile iron in HJ16 cells following hemin treatment could either be due to higher HO protein levels or lower intracellular Ft levels in HJ16 cells when compared to parental J16 cells. We therefore investigated the level of these proteins in both J16 and HJ16 cells following various treatments as detailed below.

The role of HO-1 and HO-2 in Jurkat cell lines

The higher expression of HO-1 and/or HO-2 in HJ16 cell line might contribute to accumulation of LIP levels following hemin treatment, since hemin is a known substrate for these enzymes. Previous analysis of the level of *ho-1* mRNA accumulation in J16 and HJ16 cells using the real-time PCR technique (Yiakouvaki, 2003) revealed that the basal level of *ho-1* cDNA is 2-fold higher in the H₂O₂-resistant cells than in the parental cells. Furthermore the basal level of HO-1 protein in H₂O₂ resistant cells was found to be 2-fold higher than in parental cells. So it was concluded that HO-1 expression should play a role in hemin-induced iron accumulation in HJ16 cells. Furthermore when both cell lines were treated with 20 µM hemin at various time points, a significant increase in HO-1 was only observed in

parental cell line. Yiakouvaki (2003) concluded that HO-1 protein is not inducible in HJ16 cells presumably because gradual adaptation of cells to H₂O₂ provokes a refractory response of HO-1 to hemin.

Since hemin is also a known substrate of HO-2 protein, it was important to check in our study the level of its expression in Jurkat T cells. We therefore decided to carry out an in depth study of the expression of HO-1 and HO-2 at protein levels following various treatments using Western blot analysis. Overall, these treatments were (1) Hemin/DFO alone or Hemin/DFO pre-treatment prior to H₂O₂ treatment, (2) Time-course of hemin treatment, (3) Time-course of H₂O₂ treatment, (4), Time-course of hemin pre-treatment prior to H₂O₂ treatment and (5) Hemin pre-treatment followed by with 1 mM DFO for 2 hours and finally H₂O₂ treatment.

The basal level of HO-1 was found to very low in both cell lines and the difference in expression observed by Flow cytometry could not be visualized by Western blot analysis. Furthermore the analysis showed no increase in HO-1 level in these cell lines. Studies with Jurkat T cells performed by others have also shown that HO-1 protein expression is not detectable at basal levels by Western analysis (Pae *et al*, 2004^a; Choi *et al*, 2004; Pae *et al*, 2004^b). The basal HO-2 level on the other hand was higher than HO-1 in both cell lines but it was not modulated by any of the above treatments.

To ascertain that HO protein levels were not modulated at early hours following hemin and/or H₂O₂, the HO-1 and HO-2 levels were followed in time course analysis from 0 to 18 and/or 24 h following hemin and/or H₂O₂ treatments. The results revealed that neither HO-1 nor HO-2 levels are modulated by these treatments. To complete the analysis, the levels of HO-1 and HO-2 proteins were also checked after combined hemin+DFO and/or H₂O₂ treatment. Again here, no modulation in protein levels of HO-1 and HO-2 was observed. Taken together these results showed that high iron accumulation after hemin treatment in HJ16 cells might not be related to differential expression of HO proteins in these cells.

Following oxidative stress (UVA and H₂O₂), HO-1 mRNA levels were strongly inducible in dermal fibroblasts and were barely inducible in human epidermal keratinocytes that are known to be naturally resistant to oxidative insults (Applegate *et al*, 1995). HO-2 mRNA levels on the other hand were found to be high in epidermal keratinocytes but low in dermal fibroblasts. The higher resistance of epidermal keratinocytes to UVA-induced necrotic cell death has also been linked to

the LIP, since both ‘basal’ and ‘UVA-induced’ levels in keratinocytes were several fold lower than in their matched dermal fibroblasts (Zhong *et al*, 2004).

In eight of the human cancer cells examined (Ding *et al*, 2006); HO-1 expression was not detectable in three, including Jurkat cells. Interestingly, HO-2 was highly expressed in these three cells whereas HO-1 was not present. Si-RNA-mediated knocking down of HO-1 has also been shown to increase HO-2 expression in human skin fibroblasts (Julia Zhong Li and Rex M. Tyrrell, unpublished data). These studies suggested that HO-2 may down regulate the expression of HO-1, thereby directing the co-ordinated expression of HO-1 and HO-2.

Seta *et al*, (2006) were the first to demonstrate that HO-2 is crucial in the regulation of inflammation; in the absence of HO-2, resolution of inflammation was impaired resulting in a continuous influx of inflammatory cells and subsequently, an exacerbation of cellular injury. They have also demonstrated that HO-1 function depends on the activity of HO-2, since the study indicates that in the absence of HO-2, functional HO-1 induction is impaired and HO activity is abrogated.

Both HO-1 and HO-2 break down heme as their substrate to release its iron. The excess iron is usually sensed by IRP-1 that activates the synthesis of Ft molecules to sequester the iron that would otherwise be potentially harmful to cells especially during an oxidative stress condition. In the present study the high expression of HO-2 appeared to be sufficient to break down heme to release its iron. But the fate of the released iron appeared to be different in these two cell lines and we speculated that this difference could be related to differential expression of Ft protein in these cell lines.

The role of ferritin in Jurkat cell lines

Ferritin sequesters the potentially harmful labile iron within its shells by H-Ft's ferroxidase activity so that iron could be stored in an inactive form. H-Ft has ferroxidase activity and is required for incorporation of iron *in vivo*. L-Ft (which lacks the ferroxidase centre) on the other hand, promotes nucleation of the metal inside the cavity and stabilizes the ferritin shell; it does not incorporate iron *in vivo*. Several cellular studies have shown that in oxidative stress conditions Ft could have a protective effect against oxidative damage as it removes iron that acts as a catalyst in biological oxidation (reviewed in Arosio and Levi, 2002 and Torti and Torti, 2002).

As mentioned in section 1.4.1.3, in the early stages of oxidative challenge, Ft degradation could be a potential source of iron. Cairo *et al* (1995) have suggested that liver Ft can act as a pro- or an antioxidant in a time dependant manner. An early decrease in Ft has been shown after treatment of Wistar rats with phorone, a glutathione depleting drug that amplifies the effects of ROS. Interestingly, 6-fold induction in Ft synthesis was observed as a late response. In the case of UVA and skin cells, Ft also acts as a pro- and antioxidant in a time dependent manner. Treatment of skin fibroblasts with UVA leads to an immediate degradation of intracellular Ft (Pourzand *et al*, 1999). The consequent iron release played a key role in exacerbating UVA-induced oxidative damage and led to necrotic cell death (Zhong *et al*, 2004 and Yiakouvaki *et al*, 2006). However 6 h after UVA treatment, Ft levels returned to normal and then increased thereafter up to 3-fold 24-48 hours following UVA treatment. The long term increase in Ft levels was associated with increased resistance of skin fibroblasts to subsequent UVA-induced membrane damage (Vile and Tyrell 1993).

The proteolytic degradation of Ft upon UVA irradiation of skin cells occurs as a result of damage to lysosomal membranes leading to leakage of potentially harmful lysosomal proteases to cytosol which in turn act to degrade cytosolic proteins; notably Ft (Pourzand *et al*, 1999). Studies by Brunk and co-workers (Brunk *et al*, 1995^b) have demonstrated that acute exposure of macrophage-like J-774 cells to H₂O₂ also triggers lysosomal damage. The irradiation of human fibroblasts with a moderate dose of blue light also resulted in oxidative apoptotic cell death as a result of damage to lysosomal organelles (Brunk *et al*, 1997). Damage to lysosomes was accompanied by leakage of lysosomal contents including hydrolytic enzymes, such as cathepsin D (CATH D) (Roberg and Öllinger, 1998) that should almost certainly lead to proteolytic degradation of Ft as well.

Interestingly epidermal skin keratinocytes that have low basal level of Ft and LIP are naturally resistant to UVA-induced necrotic cell death but overnight hemin treatments renders these cells vulnerable to UVA-induced peroxidative damage and necrotic cell death (Zhong *et al*, 2004). This is because iron loading of cells with hemin increases strongly the level of intracellular Ft which in turn increases the level of UVA-induced LIP upon radiation-mediated proteolysis of Ft molecules.

Since HJ16 cells' resistance to H_2O_2 was abolished after hemin treatment presumably because of high accumulation of labile iron in these cells, it was important to investigate the role of Ft in this phenomenon.

As in HO, in general the conditions for H- and L-Ft levels measurements were: (1) Time-course of H_2O_2 treatment, (2) Time-course of hemin treatment, (3) Time-course of hemin pre-treatment prior to H_2O_2 treatment, (4) Hemin/DFO alone or Hemin/DFO pre-treatment prior to H_2O_2 treatment, and (5) Hemin pre-treatment followed by with 1 mM DFO for 2 hours and finally H_2O_2 treatment.

Our results demonstrated that the 'basal' levels of H-Ft in J16 cell line are 7-fold higher than in HJ16 cell line. The lower H-Ft levels in HJ16 might be part of the adaptive response developed during gradual adaptation of these cells to H_2O_2 . As for L-Ft they had the same 'basal' level in both cell lines. However in the study carried out by Lipinski *et al* (2000), both the H- and L-Ft levels were found to be higher in the H_2O_2 -resistant cells than in the H_2O_2 -sensitive mouse lymphoma cells. The latter results differ from our study, presumably due to difference in cell type or due to difference in the regulation of iron homeostasis or the adaptive mechanism developed following chronic H_2O_2 treatment.

The time course experiment further revealed that following H_2O_2 treatment the levels of H-Ft decreased gradually in J16 cells at 6 h post treatment time point and this level remained lower than control value up to 24 h following treatment. Hydrogen peroxide treatment of cultured fibroblasts and macrophages has also been shown to significantly inhibit the synthesis of Ft (Pantopoulos and Hentze, 1995 and Mehlhase *et al*, 2005, respectively). The decrease in Ft levels has also been shown in rat liver lysates subjected to postischemic reperfusion (Tacchini *et al*, 1997). The L-Ft time course study following H_2O_2 treatment revealed that the L-Ft levels remain unchanged in J16 cells but slightly increase up to 2-fold control value in HJ16 cells at 6 h time point and then return to around control value at 24 h.

When cells were treated with 0.5 mM H_2O_2 and the Ft levels were measured *immediately*, the H-Ft level slightly decreased in J16 cells but did not affect significantly the L-Ft. The H-Ft levels in HJ16 were not significantly affected by H_2O_2 treatment, L-Ft on the other hand increased up to 3-fold of the control value. But when the cells were incubated for an additional 24 h in CM, the H-Ft decreased more in J16 cells but in HJ16 cells, the H-Ft levels remained unchanged. The H_2O_2 -mediated decrease in H-Ft levels in J16 is likely to contribute to their increased

susceptibility to H₂O₂-induced oxidative damage, since the lower Ft levels will not be able to sequester all the iron that is released by H₂O₂. Furthermore since lysosomes are severely damaged after H₂O₂ treatment in J16 cells, it is possible that the decrease in Ft levels is due to its proteolytic degradation by lysosomal proteases leaked in the cytosol. Lysosomes themselves are a known source of iron so their damage should almost certainly increase the pool of potentially harmful iron in the cytosol. It is assumed that a proportion of LIP levels detected in J16 cells following H₂O₂ treatment originates from lysosomal compartments. Similarly, Yiakouvaki (2003) has demonstrated that H₂O₂ also damages the mitochondrial membranes in J16 but not HJ16 cells, leading to intracellular depletion of ATP that contributes to H₂O₂-induced necrotic cell death observed in J16 cells. Damage to mitochondria will release the iron content of these organelles. Indeed in addition to lysosomes, mitochondria are known to contain considerable amount of iron (Petrat *et al*, 2002).

In HJ16 cells, the H-Ft levels remained unchanged following H₂O₂ treatment. Since lysosomal organelles are not significantly damaged by H₂O₂ in this cell line, it is reasonable to assume that Ft molecules remain intact in HJ16 cells and are not subject to proteolytic degradation by lysosomal proteases that leak in the cytosol in the case of J16 cells. Mitochondrial membrane was also more resistant to H₂O₂-induced oxidative damage in HJ16 cells (Yiakouvaki, 2003). The resistance of lysosomal and mitochondrial membranes in HJ16 cells will almost certainly contribute to the observed low LIP levels after H₂O₂ treatment as their compartmental LIP would not release to cytosol as a result of damage. Therefore it is reasonable to suggest that lower Ft levels in HJ16 cells is due to adaptive mechanism developed in these cells, because these cells would only show low LIP levels after H₂O₂ so the presence of high basal levels of H-Ft were redundant for the response of these cells to H₂O₂.

Unlike in our cell model, overexpression of the H-Ft increased the resistance of murine erythroid leukaemia (MEL) cells and HeLa cells to H₂O₂ treatment (Epsztejn *et al*, 1999 and Cozzi *et al*, 2000). Ferritin seems to act as a pro-oxidant molecule in J16 cells and an antioxidant in HJ16 cells following H₂O₂ treatment. The L-Ft on the other hand, was not significantly affected in J16 cells but it was slightly increased in HJ16 cells.

The treatment of cells with 100 µM DFO strongly reduced the level of H-Ft in J16 cells. In HJ16 cells, DFO treatment also decreased the level of H-Ft although to a

lesser extent than in J16 cells. The decrease in H-Ft levels by DFO is consistent with previous observations showing that DFO diminishes Ft biosynthesis in B6 fibroblasts (Pantopoulos and Hentze, 1995) and reduces Ft levels in macrophages (Mehlhase *et al*, 2005). The DFO treatment decreased significantly the L-Ft levels in J16 cells but strongly induced their levels in HJ16 cells. The reason for this increase is not clear. One explanation would be that L-Ft compensates for the strong decrease of H-Ft in HJ16 cells. Indeed Kakhlon *et al*, (2001) have reported that there is an active role of both H- and L-Ft in modulating LIP and that they both balance each other when one of them was repressed. Following the 24 h incubation in CM after the DFO treatment, H-Ft decreased further in J16 and HJ16 cells. DFO treatment of HeLa cells demonstrated nearly a total repression of Ft (Cairo *et al*, 1985), as it also significantly decreased both subunits in K562 cells (Konijn *et al*, 1999). On the other hand, the L-Ft levels decreased significantly in J16 cells but not in HJ16 cells.

The H₂O₂ treatment of DFO-treated cells, decreased even more the H-Ft levels in J16 cells and HJ16 cells. On the other hand, there was a non-significant change in the L-Ft expression in both cell lines. This was also true following the 24 h incubation in CM following DFO + H₂O₂ treatment; H-Ft was strongly decreased in J16 cells and HJ16 cells. On the other hand, the L-Ft levels remained unchanged in both cell lines. DFO is known to suppress the Ft synthesis via activation of IRP-1 binding. This has been seen for example with treatment of skin fibroblast cells with DFO (Pourzand *et al*, 1999) and in B6 fibroblasts. In the latter case the IRP/IRE binding activity was increased in B6 cells when pre-treated with DFO alone or prior to H₂O₂ treatment (Pantopoulos and Hentze, 1995).

The time course experiment following hemin treatment revealed that the increase in H-Ft levels in both the J16 and HJ16 cells was not highly induced in the early hours after treatment, presumably because Ft molecules takes time to get synthesized. However this level was increased dramatically from 8 h time point. The latter data is expected as hemin should first be broken down by HO and release its iron which in turn will stimulate *de novo* Ft synthesis. The rate of Ft synthesis in Hela cells increased only 4 h after hemin treatment (Kvam *et al*, 2000). The *de novo* synthesis of Ft in skin fibroblasts following its proteolytic degradation by UVA was also apparent from 4 h post-irradiation time point (Pourzand *et al*, 1999). The iron accumulation in HJ16 cells after hemin treatment was only apparent after 2 h post treatment with a peak at 6 h after which was then reduced, presumably because of

sequestration of a portion of it in the newly synthesized Ft molecules since this timing coincided with detection of higher Ft levels.

Overall the comparison of H-Ft levels between J16 and HJ16 after 18 h hemin treatment shows that J16 has much higher H-Ft levels than HJ16. Ferritin biosynthesis also strongly increased in B6 fibroblasts pre-treated with haem arginate (Pantopoulos and Hentze, 1995). Ferritin expression was highly induced when skin keratinocytes and fibroblasts were treated overnight with hemin (Zhong *et al*, 2004 and Reelfs *et al*, 2004). Ferritin expression was also increased 6-fold following overnight treatment with hemin in macrophages (Mehlase *et al*, 2005). A strong up-regulation of both H- and L-Ft chains was reported in HeLa cells after iron administration (Cairo *et al*, 1985). On the contrary, only H-Ft was induced after hemin treatment in bovine artery endothelial cells (Lin *et al*, 1998), L-Ft on the other hand was unaffected.

The lower H-Ft level in HJ16 cells after hemin treatment appears to be not sufficient to sequester the excess iron load by hemin, since the level of LIP remains high even after 18 h post-treatment time point. Under conditions of severe macrophage lysosomal iron overload, induction of Ft synthesis is also not enough to completely prevent the H₂O₂-mediated cytotoxicity effects (Garner *et al*, 1997). On the other hand, the higher level of H-Ft in J16 cells appears to be sufficient to incorporate the excess iron from hemin breakdown, since the LIP level were returned to control value 18 h after hemin treatment. Additional incubation of J16 and HJ16 cells for 24 h in CM following 18 h hemin treatment increased further the H-Ft levels in both cell lines although still to much lower extent in HJ16 cells.

Exposure of hemin treated cells to 0.5 mM H₂O₂ significantly increased the H-Ft and L-Ft levels in both cell lines although to a lesser extent in HJ16 cells. The presence of excess iron in HJ16 cells promoted severe oxidative damage in this cell line that led to high percentage of necrotic cell death. These results indicated that loading of HJ16 cells with iron in the form of hemin abolishes their resistance to H₂O₂. In J16 cells, induction of high H-Ft levels after hemin treatment appeared to protect the cells against H₂O₂-induced oxidative damage and necrotic cell death. So Ft molecules in J16 cells acted as an antioxidant as has been reported in some studies. For example, in endothelial cells, iron loading for 1 h significantly increased the cytotoxicity of H₂O₂ or oxidants from activated inflammatory cells (Balla *et al*, 1992). Interestingly, at 16 hrs the cells became highly resistant to oxidative-mediated injury. This was correlated with 50-fold and 10-fold increase in HO and Ft, respectively.

This has also been demonstrated in murine L1210 lymphocytic leukaemia cells using various types of oxidative insults (Lin and Girotti, 1997). Only after long-term exposure (20-24 hrs) to hemin, cells became significantly resistant to both H_2O_2 and $^1\text{O}_2$ toxicity. This observation was correlated with 12 to 15-fold increase in H-Ft. L-Ft, on the other hand, was not modified. This seems to be the case in J16 cells where Ft is acting as an antioxidant, as hemin pre-treatment prior H_2O_2 treatment promoted less necrosis. This could explain the protection that hemin has offered in J16 cells prior to H_2O_2 treatment. In HJ16 cells, the H- and L-Ft induction was highly induced to incorporate the LIP release after hemin pre-treatment, but the absolute level of H-Ft was dramatically lower than that of J16. That is why HJ16 could not cope by excess iron from hemin treatment since Ft induction was not sufficient to sequester extra iron and protect the cells from oxidative damage exerted by H_2O_2 treatment. In the latter case Ft failed to act as an antioxidant.

Finally the effect of hemin and DFO treatment with and without H_2O_2 treatment was investigated. The DFO treatment increased the level of H- and L-Ft induction after hemin treatment in both cell lines. Accordingly the level of necrotic cell death decreased in HJ16 cells after H_2O_2 treatment. The latter data confirmed that the increased susceptibility of HJ16 cells to H_2O_2 was due to high iron accumulation by hemin breakdown that could not be entirely sequestered within low amount of Ft molecules available. But additional DFO treatment cleared excess iron from the cells and therefore decreased the high level of necrotic cell death observed with hemin treatment alone. In at least six different cell lines, DFO exposure to iron pre-loaded cells accelerated Ft protein turnover in the lysosomes and consequently iron release from Ft (Truty *et al*, 2001; Kindane *et al*, 2006; De Domenico *et al*, 2006).

Mitochondrial ferritin (Mt-Ft) was also measured in both cell lines. In J16 cell line Mt-Ft basal level was 0.53 ng/mg and 1.52 ng/mg in HJ16 cells. In J16 cell line, following either hemin or DFO treatment prior H_2O_2 treatment or H_2O_2 treatment alone, Mt-Ft was negligible. On the other hand, in HJ16 cell line, Mt-Ft was increased up to 4-fold after 0.5 mM H_2O_2 treatment (measured 24 h following the treatment), overnight treatment with 20 μM hemin (measured 24 h following the treatment), H_2O_2 treatment (0.5 mM) following overnight treatment with 20 μM hemin (measured immediately following the treatment). It was also increased up to 5-fold after overnight treatment with 100 μM DFO (measured 24 h following the treatment). Mitochondrial ferritin (Mt-Ft) is currently under investigation in our cell model.

The role of iron-mediated lysosomal damage in J16 and HJ16 cells

Lysosomes have been implicated in the turnover of Ft (and consequently, iron release) in K562 cells (human leukaemia cell line) and human fibroblasts (Roberts and Bomford, 1988 and Radisky and Kaplan, 1998). Treatment of human skin fibroblasts with UVA radiation (320 – 380 nm) lead to an immediate release of iron via the proteolysis of Ft (Pourzand *et al*, 1999). This study provided the first evidence that UVA-mediated Ft degradation originates from the destabilization of lysosomal membranes and the subsequent leakage of proteolytic enzymes. Chymotrypsin, a lysosomal protease that is responsible for the degradation of Ft molecules in lysosomes, was around 3-fold higher in UVA-treated cells when compared with unirradiated controls. The degradation of Ft was prevented when cells were pretreated with Chymotrypsin-specific lysosomal protease inhibitors (i.e. Chymostatin and Leupeptin). Delocalisation of CATH B from the lysosomal compartment to the cytosol was observed after UVA radiation in human skin fibroblasts (Basu-Modak *et al*, 2006). When human skin fibroblasts were pre-treated with catechins, flavonoid constituents with protective properties predominantly against oxidative stress, prior to UVA-radiation; iron release was prevented (Basu-Modak *et al*, 2006). De Domenico *et al*, (2006) have suggested that the Ft can be degraded by two mechanisms: lysosomal degradation of Ft and a cytosolic route in which iron is extracted from Ft prior to the degradation by proteasome. It has been also demonstrated that in three different cell types [Rat hepatoma cells, human Caco2 (colonic tumour), and K562 cells] cytosolic Ft is largely degraded in the lysosomes. And that the release of iron from Ft is dependent on the degradation of Ft protein shell by lysosomal proteases (Kidane *et al*, 2006). Therefore it is well known that lysosomes contain high amounts of redox-active iron. Such iron can catalyse Fenton reactions in the presence of H₂O₂, resulting in lysosomal membrane damage and the subsequent efflux of redox-active iron and cathepsins (and other hydrolytic enzymes) into the cytoplasm (Yu *et al*, 2003 and Kurz *et al*, 2004). This efflux can lead to cell damage and ultimately cell death (either apoptotic or necrotic, depending on the magnitude of the insult). Therefore, it was decided to monitor lysosomal membrane damage in the cell model by three independent assays: (1) Neutral red uptake assay (2) Lysosensor immunofluorescence, and (3) Cathepsin B immunocytochemistry.

Overall the results clearly demonstrated that the lysosomal membranes in the parental J16 cells are very sensitive to H₂O₂ treatment, whereas in the HJ16 cells, the

lysosomal membranes were very resistant to the same treatment. In the absence of catalytically active iron neither superoxide radicals nor H_2O_2 induced any lysosomal damage by themselves, in lysosome-enriched mitochondrial fraction of a rat liver homogenate (Zdolsek and Svensson, 1993). Lysosomal rupture may occur within minutes following an oxidative stress insult, however the ultimate leakage of iron may be delayed by hours (reviewed in Kurz *et al*, 2008). In J16 cells, both DFO and hemin protected the cells from lysosomal damage (as discussed previously). This is in agreement with our previous results showing that these two compounds protected J16 cells from H_2O_2 -induced necrosis. Since DFO is a hydrophilic molecule, it cannot penetrate cellular membranes very easily. It was therefore proposed that DFO is taken up predominantly via endocytosis and localises almost exclusively within the lysosomal compartment where it seems to remain and makes the iron redox-inactive (Graf *et al*, 1984 and Lloyd *et al*, 1991). Several studies have shown the DFO can protect the cells against H_2O_2 -mediated oxidative damage (Doulias *et al*, 2003; Yu *et al*, 2003; Kurz *et al*, 2004). This therefore revealed (1) the importance of redox-active iron in the stability of lysosomes in oxidative stress and (2) H_2O_2 *per se* is not detrimental (reviewed in Kurz *et al*, 2008). In HJ16 cells, the scenario was quite different, interestingly DFO pre-treatment (unlike the necrosis data) had no significant protective effect when compared with cells treated with H_2O_2 alone. Hemin, on the other hand, promoted more lysosomal damage in HJ16. Ferric iron has been shown to be essential for the cell death of hepatocytes by H_2O_2 and the lysosomal pool seems to be the source of this iron (Starke *et al*, 1985). The lysosomal damage was also investigated in both cell lines after combined hemin-DFO treatment. It was shown that DFO treatment following iron loading for 18 h protected both cell lines from lysosomal damage. These results were in agreement with necrosis data using Flow cytometry, since combined hemin-DFO pre-treatment increased significantly the number of live cells.

Cathepsin B is one of the most abundant and widely expressed lysosomal cysteine proteases and is considered necessary for protein turnover in cells (Chapman *et al*, 1997). In the synovial fluid of RA, CATH B may participate in the joint destruction by the degradation of bone collagen (Hashimoto *et al*, 2001). It has been also reported that CATH B contributes to TNF- α -mediated hepatocyte apoptosis by promoting mitochondrial release of cytochrome *c*. Inhibition of CATH B is a mechanism by which NF- κ B protects the cells from lysosomal-mediated apoptosis

and necrosis (Liu *et al*, 2003). The results obtained from Cathepsin B immunocytochemistry confirmed the results shown with either NR or Lysosensor assays. In J16 cells, both DFO and hemin pre-treatments protected the cells against lysosomal membrane damage induced by H₂O₂. In contrast, hemin pre-treatment in HJ16 cells significantly damaged the lysosomes following H₂O₂ exposure where DFO pre-treatment had no significant effect.

Preliminary Clinical data

A preliminary study on human and rat fibroblasts were conducted in parallel of the current study. In addition to this, LPI measurements of normal, RA and OA synovial fluid (SF) were measured.

The results revealed that both HN-1 and HOA-1 cells were resistant even to high non-physiological doses of H₂O₂. The basal LIP levels of HN-1, HRA-1, and HOA-1 were very low. Because of the higher susceptibility of HOA-1 to H₂O₂-mediated damage it was hypothesised that H₂O₂-induced levels of LIP in HOA-1 would be higher than HN-1 following treatment with an intermediate dose of H₂O₂ (i.e. 1mM). The results were in agreement with our hypothesis, since following treatment of cells with an intermediate dose of 1mM H₂O₂, the LIP levels in HOA-1 increased to a detectable level (i.e. $0.18 \pm 0.06 \mu\text{M}/\mu\text{g}$) while it remained at undetectable levels in HN-1. The LIP was also undetectable in HRA-1 cells.

Normal (VW-1) and AA (AAVW-1) rat fibroblasts were also treated with the same concentrations of H₂O₂ and it was quite interesting to note that AAVW-1 cells were very resistant to all the doses used while VW-1 was very sensitive to the same treatment. The basal levels of the LIP were also undetectable in VW-1 but in AAVW-1 cells it was found to be within detectable range of $0.003 \pm 1.25 \times 10^{-5} \mu\text{M}/\mu\text{g}$. Similarly with our rat cell model, it was hypothesised that an increase in LIP will be only seen in the normal (VW-1) cells when compared to AA (AAVW-1) rat fibroblasts after H₂O₂ treatment. Following an intermediate dose of 1mM of H₂O₂, the LIP levels of VW-1 increased to the detectable levels and in AAVW-1 cells, the increase was interestingly more than 13-fold. From the above results, it seems that the increase in LIP is correlated with H₂O₂-induced cell damage. However, statistically, more clinical samples are needed to draw a proper conclusion. The culture of these synovial fibroblasts was time consuming and difficult and despite receiving appropriate number of biopsies for this thesis, we failed to keep most of

these biopsies in culture. It is therefore necessary to set up in the future new improved culture conditions to be able to provide satisfactory answers to the questions asked in this thesis.

Spectrographic studies showed that synovial fluid (SF) from patients with RA contained elevated concentrations of iron when compared with normal subjects (Niedermeier *et al*, 1962). By emission spectrometric analysis, the mean concentration of iron was higher in the SF of RA patients than normal subjects (Niedermeier and Griggs, 1971). Using a colorimetric method, plasma iron in RA and OA patients were non-significantly lower (p value > 0.05) than healthy subjects (Yazar *et al*, 2005). On the other hand, iron in the SF was significantly higher in OA patients than RA and healthy subjects. Ferritin levels were significantly higher in the SF of RA patients when compared with OA patients (Ahmadzadeh *et al*, 1990).

Labile iron (LI) was measured in the synovial fluid (SF) of normal, rheumatoid arthritic (RA), and osteoarthritic (OA) patients. Synovial fluid from a normal, two RA, and six OA patients was analysed. The results showed that there was no consistent pattern in these fluids. The LPI of the normal patient was $0.45 \pm 0.3 \mu\text{M}$, it seems to be slightly higher in RA but it was non-significant (p value > 0.05). In OA samples, some had higher value than the normal sample and others had lower values, but they were all non-significant. Clearly, more samples are needed to complement these observations and to draw a proper conclusion.

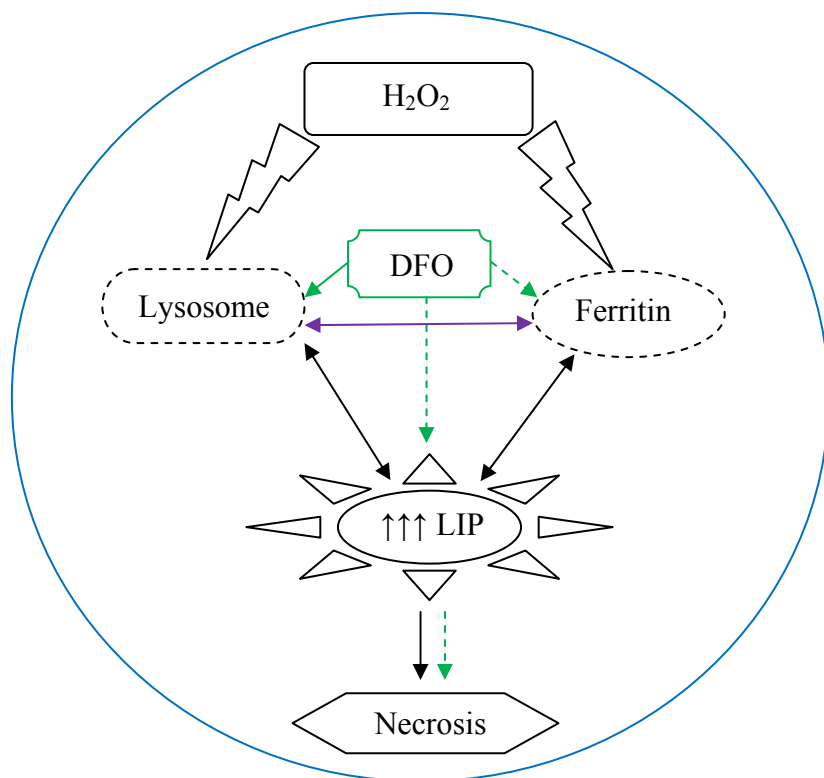
Concluding Remarks and Limitations of this study

A model of the major findings in this thesis is demonstrated in figures 4.1 and 4.2. Figure 4.1 provides a summary of the effect of H₂O₂ treatment alone or following *iron chelation* in J16 and HJ16 cells in regard to the LIP levels, lysosomal damage, the influence on Ft synthesis/decrease, and the ensuing necrotic cell death. Figure 4.2 provides a summary of the effect of H₂O₂ treatment alone or following *iron loading* in J16 and HJ16 cells in regard to the LIP levels, lysosomal damage, the influence on Ft synthesis/decrease, and the ensuing necrotic cell death. Since the Ft levels were not modulated in HJ16 cells following H₂O₂ treatment, the source of labile iron could generally be from the lysosomal damage shown in HJ16 cells.

Overall the findings of this thesis revealed that the resistance of HJ16 cells to H₂O₂ was mainly related to higher total intracellular glutathione content, higher GPx activity and lower Ft levels than J16 cells. These results strongly suggest that both antioxidants and H₂O₂-induced labile iron are modulated when cells are chronically exposed to H₂O₂. The modulation of intracellular LIP and glutathione content appears to directly influence the susceptibility of cells to H₂O₂-induced oxidative damage and necrotic cell death. These results are consistent with the conclusion that both antioxidant defence mechanisms and labile iron status are important factors to consider in oxidative injuries and in related pathological conditions such as RA. Indeed, during the progression of RA in joints, the synovial cell components notably T-cells and fibroblasts are constantly exposed to high levels of ROS that are generated during ischemia-reperfusion in response to inflammation. The chronic exposure of synovial cells to ROS should almost certainly modulate the intracellular antioxidant defence mechanism of cells; however to our knowledge, no study has investigated this phenomenon in detail. Furthermore, studies carried out by our laboratory and others (e.g. Breuer *et al*, 1997) have clearly demonstrated that acute exposure of cells to oxidising agents such as UVA or H₂O₂, promotes an increase in potentially harmful labile iron in the cells that acts to exacerbate the ongoing peroxidative cell damage, leading to necrotic cell death. However no study has explored this important phenomenon in chronic oxidative conditions such as RA. In order to gain insight into the adaptation of synovial cell components to chronic oxidative exposure in RA, it is necessary to study the behaviour of synovial fibroblast, macrophages and T-cells to both acute and chronic exposure to oxidising agents such as H₂O₂.

A. J16 cell line

In J16 cells, H_2O_2 decreases the ferritin levels and causes damage to the lysosomal membrane. This has been correlated with an increase in LIP levels and the ensuing necrotic cell death. DFO pre-treatment prior to H_2O_2 protects the lysosomal membrane and decreases the ferritin levels. This has been correlated with a decrease in the LIP levels and the ensuing cell death.

**B. HJ16 cell line**

In HJ16 cells, H_2O_2 does not significantly modulate the ferritin levels but causes damage to the lysosomal membrane to a lesser extent than in the J16 cells. This has been correlated with an increase in LIP levels and the ensuing necrotic cell death. DFO pre-treatment prior to H_2O_2 has no significant effect on lysosomal membrane but decreases the ferritin levels. This has been correlated with a decrease in the LIP levels and the ensuing cell death.

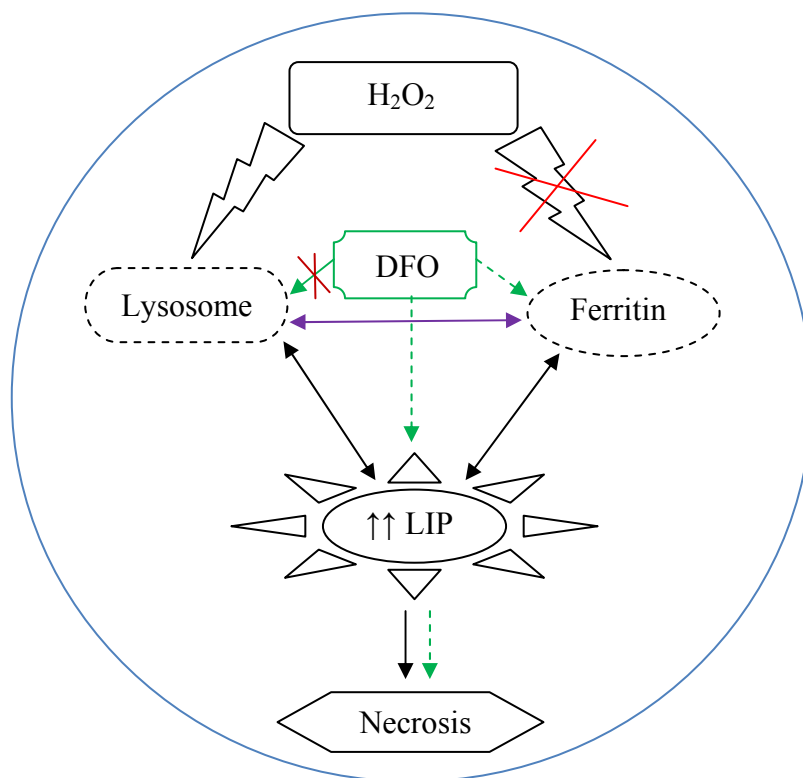
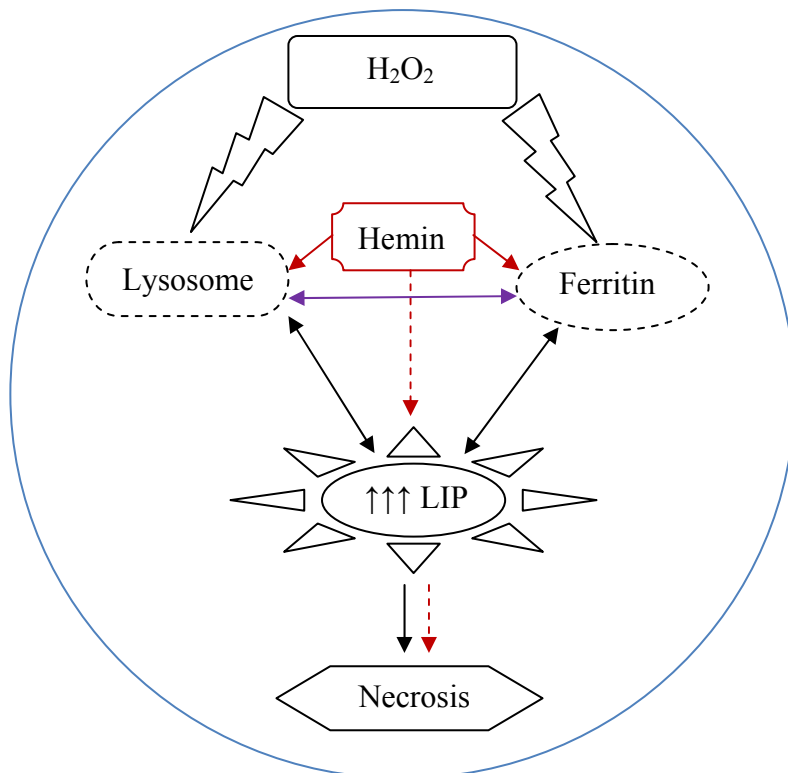


Figure 4.1 : Effect H_2O_2 alone or following iron chelation in J16 and HJ16 cells.

Protection/increase is represented by a solid line - Degradation/decrease is represented by a dashed line, and the upper arrow represents the fold increase of LIP compared with the basal levels). Lysosomes may have been implicated in the degradation of ferritin. The green colour indicates the effect of DFO pre-treatment.

A. J16 cell line

In J16 cells, H_2O_2 decreases the ferritin levels and causes damage to the lysosomal membrane. This has been correlated with an increase in LIP levels and the ensuing necrotic cell death. Hemin pre-treatment prior to H_2O_2 protects the lysosomal membrane and increases the ferritin levels. This has been correlated with a decrease in the LIP levels and the ensuing cell death.

**B. HJ16 cell line**

In HJ16 cells, H_2O_2 does not significantly modulate the ferritin levels but causes damage to the lysosomal membrane to a lesser extent than in the J16 cells. This has been correlated with an increase in LIP levels and the ensuing necrotic cell death. Hemin pre-treatment prior to H_2O_2 increased the lysosomal membrane damage and the ferritin levels. This has been correlated with an increase in the LIP levels and the ensuing cell death.

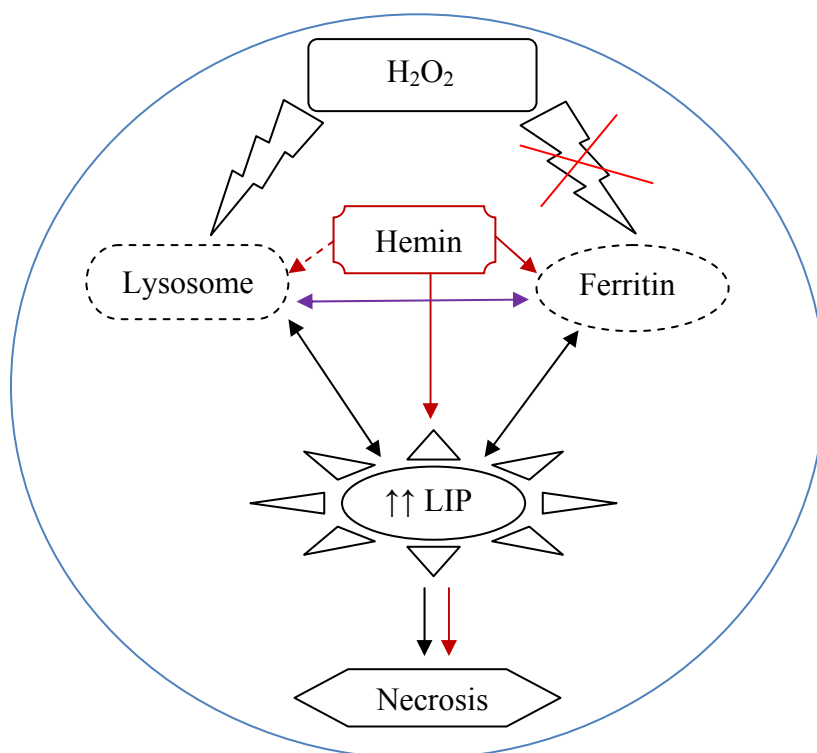


Figure 4.2 : Effect H_2O_2 alone or following iron loading in J16 and HJ16 cells.

(Protection/increase is represented by a solid line - Degradation/decrease is represented by a dashed line, and the upper arrow represents the fold increase of LIP compared with the basal levels). Lysosomes may have been implicated in the degradation of ferritin. The red colour indicates the effect of hemin pre-treatment.

Lymphocytes and macrophages are the predominant cells in chronic inflammation (Junqueira *et al*, 1986; Underwood, 1996; Stevens and Lowe, 1999). Lymphocytes are also the key components in the onset and exacerbation of autoimmune diseases and the cytokines produced by them have a great impact on disease progression (Horwood, 2008). Infiltration of numerous T-cells has been noticed in the RA synovium; T-cells represent 40% of the synovial cellular infiltrate (Ling and Miossec, 2007). Chronic inflammation occurs in an autoimmune disease (e.g. RA) in which self-antigens continually activate T-cells (Goldsby *et al*, 2003). Macrophages, fibroblasts, and T lymphocytes are three cell populations which are found abundantly in the rheumatoid arthritic synovium (Tran *et al*, 2005). T-cells can stimulate both macrophages and fibroblasts to produce more pro-inflammatory cytokines. T-cells can exert potentially pathogenic effects through their ability to modulate the functions of the surrounding cells by cell to cell contact (e.g. macrophages) or through the release of soluble factors (e.g. IL-17 on fibroblasts). Indeed, activated synovial T cells are key initiators and orchestrators of inflammation in RA, and therefore they represent key cellular targets for therapy (Cope *et al*, 2007).

Several studies have attempted to isolate synovial T-cells and macrophages to study e.g. the role of NF κ B in rheumatoid arthritis conditions, but these cells have a short half-life in laboratory-based cell culture conditions and as a result can not be used for in-depth long term studies. Furthermore the isolation of these cells in RA is subject to patient to patient differences and most importantly in such studies the lack of a ‘proper control’ should severely hamper the interpretation of the data obtained. The use of Jurkat parental T-cells (i.e. J16 cell line) in the present study provided us with such ‘proper control’ for the effects seen in its H₂O₂-adapted counterpart (i.e. HJ16 cell line). Jurkat cells are widely used in the study of T-cell activation processes (Schreck *et al*, 1991) as these cells are considered as critical determinants of the extent and chronicity of an inflammatory response. Furthermore Jurkat T-cells are particularly vulnerable to oxidative stress and therefore could illustrate clearly the nature of oxidative damage in cells upon acute exposure to oxidative stress. On the other hand, the H₂O₂-adapted cell line provides a precious tool to undertake an in-depth long term comparative study in terms of adaptation of T-cells to chronic exposure. Unpublished data from N.D Hall’s laboratory (Department of Pharmacy and Pharmacology, University of Bath) have shown that HJ16 cells have characteristics similar to those of rheumatoid synovial T cells. These characteristics

include low CD3 levels, elevated CD69 expression, increased intracellular glutathione levels, and enhanced resistance to apoptosis. They have also noticed that HJ16 cells can stimulate monocytes to secrete pro-inflammatory cytokines (i.e. IL-1 β). Although Jurkat cells are not the same as T-cells (otherwise they would not be immortal) in regard to the biochemistry, they are compromised in the study of T-cell function. HJ16 cells were derived by treating the J16 cell line with increasing concentration of H₂O₂ (i.e. from 0.1 mM to 3 mM) at weekly to fortnightly intervals. After each treatment the surviving cells were allowed to recover normal growth characteristics before further exposure to a higher concentration of H₂O₂. Although they were resistant up to a dose of 3mM H₂O₂, at 0.1 mM around 30 % of the cells were dead. The reason may be that the HJ16 cell line is a polyclonal cell line and therefore within its population, it will still contain some fraction of cells with higher susceptibility to H₂O₂ doses used.

The outcome of this study was intended to be checked in synovial fibroblasts obtained from OA and RA patients, so that the study could verify a series of parameters such as the level of antioxidant systems and the labile iron status as well as their level of resistance to H₂O₂ doses applied. As it can be seen in section 3.5, we encountered serious problems in maintaining the synovial fibroblast biopsies in culture and therefore the study lacked a proper end-point for a direct link between the effects observed in the Jurkat cell model and RA/OA cell components. Nevertheless, although our clinical samples were not studied extensively, it appears that synovial fibroblasts were very resistant to H₂O₂ and that iron is implicated in their resistance. Since synovial fibroblasts are the major source of proteases involved in tissue damage in RA, it is expected that an alteration in iron homeostasis would occur and that the potential relevance of iron chelation would be beneficial. The present thesis brings a new dimension to the role of iron in rheumatoid arthritis.

Our results raise the hypothesis that cells chronically exposed to oxidative stress as anticipated in the RA environment can withstand high and continuous levels of free radicals due to the modulation of both the antioxidants and the oxidative stress-induced iron release. It could be predicted that the high iron concentration shown in RA in the cells or in the synovial fluid arises from the lysosomal membrane damage, and/or degradation of Ft, and/or mitochondrial damage, and/or nuclear damage occurring subsequent to the oxidative stress. However, more

investigations are needed to complement the observations revealed in the Jurkat T cell lines (i.e. J16 and HJ16 cell lines) and to draw a proper conclusion.

Further Directions

The present study provided a potential link between iron, lysosomal-membrane damage and the ensuing necrotic cell death that will almost certainly help to understand their role in progression of iron- related chronic inflammatory disorders such as RA. However it is clear that more in depth investigations are required to unravel the role of Ft in chronic oxidative stress/ inflammatory conditions. Metabolic labelling of Ft and immunoprecipitation with a pulse chase experiment would be very useful in knowing if there was a difference in the half-life of Ft and if there was any difference in its processing in both cell lines. Mitochondrial iron and ferritin would be an important area to look into as Mt-Ft has the potential of being an iron regulator in the cell and to protect the mitochondria from iron-induced damage. Preliminary findings indicate the cells overexpressing Mt-Ft (i.e. HJ16 cells) are more resistant to oxidative damage induced by H_2O_2 , but obviously additional studies are required. It would be useful to measure the lysosomal proteases and to use their inhibitors and the lysosomal-membrane stabilisation compounds. Although this study has been useful to unravel some of the mechanisms and factors that might have lead to the resistance of HJ16 cells, more investigations are required: for example, to examine the TfR levels by Western blotting, ferroportin levels, human poly (rC)-binding protein (PCBP1), and the IRP/IRE system in our cell model. It will be important to look at the activity of the ferroxidase site in the H-Ft. This will hopefully lead to a better understanding of the high LIP levels measured after iron loading in HJ16 especially after the study of the radiolabel incorporation of iron. In addition to this, the effect of acute (i.e. 1-2 h) iron loading prior to oxidative stress would be an important area to explore. In the process of this study, iron loading was achieved by using haem iron since it is the most physiological source of iron, however it would be interesting to examine the effects of other sources of iron such as ferric chloride to increase lysosomal iron or ferric ammonium citrate to increase extracellular iron. The use of HO-1 and HO-2 siRNA could also provide more clues as to the role of HO in these cell lines. Moreover, the role of iron in NF κ B activation should be interesting to investigate. The role of thioredoxin is ill-defined in our system and it is important in

the future to investigate the role of this key molecule in redox regulation of genes and its role in iron metabolism.

To mimic an inflammatory environment it is necessary i.e. to combine the H₂O₂ treatment with cytokines (e.g. IL-1 β and TNF- α) in our cell model so that the effects mimic closely the *in vivo* condition. Measurements of cytokines in these cell lines after relevant treatments would be an interesting area to explore. A completion of the *in vitro* studies is also essential with the human and rat samples to further characterise them in respect to the current findings in our cell lines. It would be also beneficial to harvest and study lymphocytes from RA patients and compare the results obtained from this study. The culture of these synovial fibroblasts from patients were time consuming and difficult and despite receiving appropriate number of biopsies for this thesis, we failed to keep most of these biopsies in culture. It is therefore necessary to set up in the future new improved culture conditions to be able to prevent the contamination of the biopsies and cells. This will hopefully increase our understanding of what is occurring in RA cells.

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